

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2001, 05:33:23 ; Search time 15.69 Seconds
(without alignments)
1063.239 Million cell updates/sec

Title: US-09-599-400A-9
Perfect score: 1231
Sequence: 1 MGLSTVPDLLPLVLELLV.....ENVKCTEDSGTTLPLVLRP 219
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1219	99.0	455	1 GORUT1	tumor necrosis fac
2	906.5	73.6	461	2 JC4302	tumor necrosis fac
3	879.5	71.4	454	1 GOMST1	tumor necrosis fac
4	867	70.4	461	1 GORTT1	tumor necrosis fac
5	216.5	17.6	435	2 I54182	tumor necrosis fac
6	202	16.4	427	1 GORUN	nerve growth facto
7	200	16.2	326	1 GQV2ML	T2 protein - myxom
8	189	15.4	325	2 B43692	T2 protein - rabbl
9	188	15.3	425	1 A26431	nerve growth facto
10	181	14.7	474	2 B38634	tumor necrosis fac
11	180.5	14.7	327	2 A46484	apoptosis-mediatin
12	176	14.3	459	2 I48854	gene murine tumour
13	174	14.1	305	2 A46476	B cell-associated
14	166.5	13.5	349	2 D72175	G2R protein - vari
15	164	13.3	348	2 T28623	hypothetical prote
16	164	13.3	349	2 D36858	gene G4R protein -
17	162.5	13.2	461	1 A35356	tumor necrosis fac
18	159.5	13.0	416	1 JN0006	nerve growth facto
19	154	12.5	677	2 C42125	trophozoite cysteal
20	153.5	12.5	324	2 JC2395	Fas antigen precu
21	148	12.0	277	2 A60771	B-cell activation
22	143.5	11.7	1680	2 A43434	furin (EC 3.4.21.7
23	143	11.6	250	1 A49053	CD27 antigen precu
24	139.5	11.3	260	1 A46517	CD27 antigen precu
25	138	11.2	314	2 I37383	FAS soluble protei
26	137.5	11.2	335	2 A40036	apoptosis-mediatin
27	137.5	11.2	1548	2 S34583	serine proteinase
28	135.5	11.0	595	2 A42086	CD30 antigen precu
29	135	11.0	272	2 I48700	gene ox40 protein

30	132	10.7	899	2	G02428	subtilisin-like pr
31	132	10.7	915	2	JC6148	subtilisin-like pr
32	130.5	10.6	3672	2	T23433	hypothetical prote
33	130.5	10.6	3704	2	T37316	probable laminin a
34	126.5	10.3	271	2	S12783	Ox40 antigen precu
35	126.5	10.3	728	2	A48830	probable transcrip
36	124.5	10.1	277	2	T37552	Ox40 homolog - hum
37	122.5	10.0	192	2	T25513	hypothetical prote
38	121.5	9.9	1299	2	T43251	furin (EC 3.4.21.7
39	121	9.8	2321	2	S78549	notch3 protein - h
40	119	9.7	2318	2	S45306	notch 3 protein -
41	118.5	9.6	557	2	A48434	variant-specific s
42	118	9.6	596	2	A45664	variant-specific s
43	118	9.6	837	2	S43656	furin (EC 3.4.21.7
44	118	9.6	1790	1	NMFFB1	laminin beta-1 cha
45	118	9.6	2824	2	T22759	hypothetical prote

ALIGNMENTS

RESULT 1

GORUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence-revision 30-Jun-1992 #text-change 08-Dec-2000
C:Accession: A38208; A34899; A34900; A36555; A38281; S12057; JT0758; A60231;
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to
A:Reference number: A38208; MUID:92250049
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PI
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Less
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A:Reference number: A34899; MUID:90235284
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOB>
A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A:Experimental source: placenta
A:Note: part of this sequence, including the amino end of the mature protein, confirm
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A:Reference number: A34900; MUID:90235285
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M733294; NID:g339744; PIDN:AAA03210.1; PID:g339745
A:Residues: 1-455 <SCH>
R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A36555; MUID:91090841
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 30-38;41-53, 'X', '55-79, 'XX', '82-94, 'NK', 'XX', '100-104;107-128;162-167, 'X',16
A:Note: the purified protein, called tumor necrosis factor binding protein, is a solu
R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A:Reference number: A38281; MUID:91017509
A:Accession: A38281
A:Molecule type: mRNA

A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
A:Note: The authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
I form of the receptor.
A:Reference number: S12057; MUID:91006021
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <NQP>
A:Cross-references: EMBL:X55133; NID:g37223; PIDN:CAA39021.1; PID:g37224
A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R:Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A:Reference number: J70758; MUID:94085779
A:Accession: J70758
A:Molecule type: DNA
A:Residues: 1-113 <REM>
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
A:Reference number: A60231; MUID:90292116
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
tients.
A:Reference number: A38258; MUID:91062364
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyseil, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1989
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
A:Reference number: A60594; MUID:89171156
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A:Reference number: A35010; MUID:90110215
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
R:Kajihara, J.; Asada, K.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
A:Reference number: J02404; MUID:95128033
A:Accession: J02404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Experimental source: urine
A:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.3
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
A:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence status predicted <SIG>
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
F:30-211/Domain: extracellular status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F:44-82/Domain: NGF receptor repeat homology <NGF>

F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.2e-82;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPQNNISICT 60
Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPQNNISICT 60

Qy 61 KCHKGTYLYNDPCPGQDTCRECESGSFTASENHLRHLCSCKRKGVEISSCTVD 120
Db 61 KCHKGTYLYNDPCPGQDTCRECESGSFTASENHLRHLCSCKRKGVEISSCTVD 120

Qy 121 RDTVCGCRKQYRHYWSENFQCFNCSLCLNGTVHLSOERKONTVCTCHAGFFRENECV 180
Db 121 RDTVCGCRKQYRHYWSENFQCFNCSLCLNGTVHLSOERKONTVCTCHAGFFRENECV 180

Qy 181 SCNSCKSLECTKLCPLQIENVKGTEDSGTIVLLPLV 217
Db 181 SCNSCKSLECTKLCPLQIENVKGTEDSGTIVLLPLV 217

RESULT 2
JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A:Reference number: JC4302; MUID:96011645
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NGF>
F:211-231/Domain: transmembrane #status predicted <TMM>
F:361-447/Domain: signal transduction #status predicted <SIT>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.6%; Score 906.5; DB 2; Length 461;
Best Local Similarity 74.7%; Pred. No. 3.2e-59;
Matches 162; Conservative 16; Mismatches 38; Indels 1; Gaps 1;

Qy 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPQNNISICT 60
Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKDSVCPQGYIHPQNNISICT 60

Qy 61 KCHKGTYLYNDPCPGQDTCRECESGSFTASENHLRHLCSCKRKGVEISSCTVD 120
Db 61 KCHKGTYLYNDPCPGQDTCRECESGSFTASENHLRHLCSCKRKGVEISSCTVD 120

F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAY>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-136/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.4%; Score 879.5; DB 1; Length 454;
Best Local Similarity 71.6%; Pred. No. 3e-57;
Matches 156; Conservative 23; Mismatches 38; Indels 1; Gaps 1;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKRDSCVPGQKYIHPQNNISICT 60
DB 1 MGLTPVGLLSLVLLALLMGIIHPSGVIGLVPLGLDRKRDSCVPGQKYVHKNNSICT 60

QY 61 KKHGKTYLYNDPCPGQGDTCRECESGSFTASENHLRHLSCSKORKEMGQVEISSCTVD 120
DB 61 KKHGKTYLYNDPCPGQGDTCRECESGSFTASENHLRHLSCSKORKEMGQVEISSCTVD 120

QY 121 RDTVCGCRKNQYRHYWSENFLPQCFNCSLCLNGTVHLSQERKQNTVCTCHAGFFLENECV 180
DB 121 RDTVCGCRKNQYRHYWSENFLPQCFNCSLCLNGTVHLSQERKQNTVCTCHAGFFLENECV 180

QY 181 SCNSCKSLECTKLCCL-POIENWKGTEDSGTVTLVLLPLV 217
DB 181 PCSCKKNECKKLCPLPPPLANVTNPQDSGTAVLLPLV 218

RESULT 4
GORTT1
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: B36555
R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; La
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor
A;Reference number: A36555; MUID:91090841
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HTM>
A;Cross-references: GB:M63122; NID:g207361; PID:AAA42256.1; PID:g207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAY>
F;30-211/Domain: extracellular #status predicted <EXT>
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TB>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-136/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;213-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.4%; Score 867.; DB 1; Length 461;
Best Local Similarity 70.0%; Pred. No. 2.5e-56;
Matches 152; Conservative 21; Mismatches 44; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKRDSCVPGQKYIHPQNNISICT 60
DB 1 MGLTPVGLLSLVLLALLMGIIHPSGVIGLVPLGLDRKRDSCVPGQKYVHKNNSICT 60

QY 61 KKHGKTYLYNDPCPGQGDTCRECESGSFTASENHLRHLSCSKORKEMGQVEISSCTVD 120
DB 61 KKHGKTYLYNDPCPGQGDTCRECESGSFTASENHLRHLSCSKORKEMGQVEISSCTVD 120

A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31,'V',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>
A;Experimental source: melanoma cell line A875
A;Note: This sequence has been corrected by a note added in proof to follow the nucle
R;Vissavajhala, P.; Leszyk, J.D.; Lin-Coerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor
A;Reference number: S21689; MUID:92198017
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor recept
A;Reference number: I57638; MUID:89096903
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
C;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C;Comment: The cysteine-rich region of the extracellular domain may form part or all
C;Comment: This protein is thought to form a high-affinity receptor when it associate
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-427/Product: nerve growth factor receptor #status experimental <NAT>
F:23-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NGL>
F:67-108/Domain: NGF receptor repeat homology <NG2>
F:109-147/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Region: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TRM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) #status predicted

Query Match 16.4%; Score 202; DB 1; Length 427;
Best Local Similarity 29.98%; Pred. No. 7.5e-08;
Matches 61; Conservative 30; Mismatches 78; Indels 36; Gaps 12;

Qy 12 PLVLLELLVGIYTPSGTGLVPHLGDKREKRSVCPQGRKYIHQNNSICTKCHKGTLYLND 71
Db 13 PRLLLLLLGVSLGA-----KEAFTGLYTH---SGECKKACNLGEGVAQP 56
Qy 72 CPGPQDTCREC-ESGSFTASENHLRCLSCSKCKEMQVEISS-CTVDRTFVCGCRK 129
Db 57 C-GANQ-TVCEPLCDSTVTFSDVSATEPCPKPCTEC---VGLQSMSAPCVDADDVAVCR-- 109
Qy 130 NQRYHWSNLFQCFNCSCLNGT-VHLSQERKONTYC-TCHAGFFLRE---NECVSCS 183
Db 110 -AYGYQDETGTGRCAECVCEAGSLVFSCODKQNTVCEECPDGTYSDANHVDPLPCT 168
Qy 184 NC-----KKSLCTKLCPLQIENVKG 204
Db 169 VCDTERQLRCECTRWADAECEEPG 193

RESULT 7
GOVZML
T2 protein - myxoma virus (strain Lausanne)
C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A40566
R;Upton, C.; Maceen, J.L.; Schreiber, M.; McFadden, G.

Virology 184, 370-382, 1991
A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor
A:Reference number: A40566; MUID:91335768
A:Accession: A40566
A:Molecule type: DNA
A:Residues: 1-326 <UPT>
A:Cross-references: GB:M95181; GB:M37976; NID:9332309; PIDN:AAA46632.1; PID:9332310
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
C:Keywords: glycoprotein
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.2%; Score 200; DB 1; Length 326;
Best Local Similarity 25.8%; Pred. No. 8.6e-08;
Matches 62; Conservative 28; Mismatches 88; Indels 62; Gaps 10;

QY 14 VLLELLVGIYPSGIVGLVPHLGDREKRDVCPQGYIHPQNNISICCTKCHKGTLYNDP 73
DB 6 LLLAYVACVYGGG---APYGDGRK---CRGNDY---EKDGLCCTSCPPGSVASRLC- 53
QY 74 GPGODTDCRECSGFTASENHLRHCLSC-SKCRKEMQVEISSCTVDRTVCGCRKNQY 132
DB 54 GPGSDTVCSCKNETFTASTNHAPACVSCRGCTGHLN--ESQSCDTRDRVCDCSAGNY 111
QY 133 -----RHVSENLFQCFNCSLCLNG- 152
DB 112 CLLKGQECRICAPKTKCPAGYGVSHTRGDVLCTKPRTYIDAVSSTETCTSSFNVI 171
QY 153 TVHLSQOEKQNTVCTCHAGFFLRENECVSCNCKKL---ECTKLCLPQIENVRGTEDSG 209
DB 172 SVEPNLYPVNDTCTTAG-----PNEVKTSEFVTLNHTDCDPVFHYEYGTSSSEGAG 227

RESULT 8
B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus, Shope fibroma virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: B43692
R:Opton, C.; DeLange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID:87321103
A:Accession: B43692
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 15.4%; Score 189; DB 2; Length 325;
Best Local Similarity 27.7%; Pred. No. 5.4e-07;
Matches 57; Conservative 25; Mismatches 82; Indels 42; Gaps 10;

QY 9 LLLPLVLELLVGIYPSGIVGLVPHLGDREKRDVCPQGYIHPQNNISICCTKCHKGTLY 68
DB 1 MLRLIALLVCVVYGGD---VPYSSNOGR-----CGGHDY---EKDGLCCASCHPGFYA 49
QY 69 YNDPCPGQDPTDCRECSGFTASENHLRHCLSC-SKCRKEMQVEISSCTVDRTVCGC 127
DB 50 SRLC-GPGSNVTVCSPCEDGTFTASTNHAPACVSCRGCTGHLN--ESQPCDTRDRVCNC 106
QY 128 RKNQYRHVSENLFQCFNCSLCLNGTVHLSQOEKQNTVCTCHAGFFLRENECVSCNCK 187
DB 107 STGNYCLLKGQN-----GCRICAPQT-----KCPAGYGVSGHTRAGDTLCEK 148
QY 188 SLECTKLCLPQI--ENVKGTEDSGTT 211

DB 149 -----CPPHTYSDLSLSPTRCGTS 167

RESULT 9
A26431
nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: GB:X05137; NID:956755; PIDN:CAA28783.1; PID:956756
R:Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retin
A:Reference number: PH1229; MUID:93077038
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <NET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C:Comment: The cysteine-rich region of the extracellular domain may form part or all
C:Comment: This protein is thought to form a high-affinity receptor when it associate
C:Genetics:
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <EXT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Region: serine/threonine-rich
F:252-273/Domain: transmembrane #status predicted <MEM>
F:274-425/Domain: intracellular #status predicted <INT>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.3%; Score 188; DB 1; Length 425;
Best Local Similarity 28.6%; Pred. No. 7.8e-07;
Matches 58; Conservative 30; Mismatches 79; Indels 36; Gaps 12;

QY 14 VLLELLVGIYPSGIVGLVPHLGDREKRDVCPQGYIHPQNNISICCTKCHKGTLYNDP 73
DB 16 LLLLLILGVSSGGA-----KFTCTGTGLYTH---SGECKACNLGEGVAQC- 58
QY 74 GPGQDPTDCREC-ESGFTASENHLRHCLSCSKCRKEMQVEISS-CTVDRDVTVCGRKNQ 131
DB 59 GANQ-TVCEPLDNTVFSVDVSAPECKPCTEC---LGLQMSAPCVREADDVCR- ---A 111
QY 132 YRHYWSENLFQCFNCSLCLNGT-VHLSQOEKQNTVC-TCHAGFFLRE----NECVSCSNC 185
DB 112 YGYODEETGHCACSVCEVSGSLVFCQDKQNTVCECEGPEGTYSDEANHVDPCLPCTVC 171
QY 186 ----KKSLECTKLCLPQIENVK 204
DB 172 EDTERQLRECTPWADAECCEIPG 194

RESULT 10
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: B38634; A40254; S54816

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor genes
 A:Reference number: A38634; MUID:91187885
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEW>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for A:Reference number: A40254; MUID:91246168
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Kisssomergis, M.; Fellows, R.; Feldmann, M.; Chernaiovsky, Y. submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
 A:Reference number: S54816
 A:Accession: S54816
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <KIS>
 A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG1>
 F:79-120/Domain: NGF receptor repeat homology <NG2>
 F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 14.7%; Score 181; DB 2; Length 474;
 Best Local Similarity 31.7%; Pred. No. 2.7e-06;
 Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;
 QY 44 CPQGYIHPNNISCTCKHKYLYNDPCPGQDTCRECSGSTASENHLRHCLSC- 102
 DB 40 COISQEIYDRKAQMCCKAPPGQYKHF- NKTSDPTVCADCEASMTQVWNOFRTCLSCS 98
 QY 103 SKCRKEMQVEISSTVDRDTCGCKKNQY----RHYWSENLFQCFNCSLCLNG-TVHLS 157
 DB 99 SSCYTD--QVETRACTKQNRVCACEAGRYCALKTH--SGSCRCQMRSLKCGPGFGVASS 154
 QY 158 COEKQNTVC-TCHAGFFLRENECVSCNCKSLCTKLCPLP 197
 DB 155 RAPNGNVLCKACAPGTF--SDTTSSDTCVCRPHRICSLAIP 193

RESULT 11
 A46484
 A:Title: apoptosis-mediating membrane-associated polypeptide Fas - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A46484; A47254
 R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J. Immunol. 148, 1274-1279, 1992
 A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas and A:Reference number: A46484; MUID:92148151
 A:Accession: A46484
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-327 <WAT>
 A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
 A:Experimental source: BM3 macrophage cell line
 A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)
 R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S. Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
 A:Title: Aberrant transcription caused by the insertion of an early transposable element A:Reference number: A47254; MUID:93189576
 A:Accession: A47254

A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-96 <ADA>
 A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
 A:Experimental source: MRL lpr/lpr
 A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1268 F:44-79/Domain: NGF receptor repeat homology <NGF>
 F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 14.7%; Score 180.5; DB 2; Length 327;
 Best Local Similarity 25.9%; Pred. No. 2.3e-06;
 Matches 55; Conservative 24; Mismatches 94; Indels 39; Gaps 7;
 QY 10 LLPVLLELLVGIYPSVIGLVPHLGDREK---RDSVCPQGYIHPQNNISCTCKHKGT 66
 DB 7 VLPVLVAGSOLRVHTQGTNSISLKLRRVHETDKNCSEGLY---QGGPFCCQCPQPK 63
 QY 67 YLYNDPCPGQDTCRECSGSTASENHLR-HCLSCSKCRKEMQVEISSTVDRDTCV 125
 DB 64 KVEDCKRMNGGTPTCAPCTEGKEYMDKNHYADKRCRCTLCDDEHGLEVTNCTLTQNTK 123
 QY 126 GCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCOEKQNTVCTCHAGFFLRENECVSCN 185
 DB 124 KCRPFYCD--SPGCEHCVCRCACHEGTL- PCTATSN-----NC 161
 QY 186 KKSLECTKLCPLQIENVKGTEDSGTTLPLV 217
 DB 162 RKOSPRNRLWLLTI-----LVLLIPLV 183

RESULT 12
 I48854
 A:Title: gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C:Accession: I48854
 R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A. Mamm. Genome 5, 726-727, 1994
 A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
 A:Reference number: I48854; MUID:95178848
 A:Accession: I48854
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-459 <RES>
 A:Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 14.3%; Score 176; DB 2; Length 459;
 Best Local Similarity 31.1%; Pred. No. 6.2e-06;
 Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;
 QY 44 CPQGYIHPNNISCTCKHKYLYNDPCPGQDTCRECSGSTASENHLRHCLSC- 102
 DB 25 COISQEIYDRKAQMCCKAPPGQYKHF- NKTSDPTVCADCEASMTQVWNOFRTCLSCS 83
 QY 103 SKCRKEMQVEISSTVDRDTCGCKKNQY----RHYWSENLFQCFNCSLCLNG-TVHLS 157
 DB 84 SSCSTD--QVETRACTKQNRVCACEAGRYCALKTH--SGSCRCQMRSLKCGPGFGVASS 139
 QY 158 COEKQNTVC-TCHAGFFLRENECVSCNCKSLCTKLCPLP 197
 DB 140 RAPNGNVLCKACAPGTF--SDTTSSDTCVCRPHRICSLAIP 178

RESULT 13
 A46476
 A:Title: B cell-associated surface molecule CD40, long splice form - mouse
 C:Species: Mus musculus (house mouse)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C/Accession: A46476; A46515
R/Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A/Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A/Reference number: A46476; MUID:92105763
A/Accession: A46476
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-305 <TOR>
A/Cross-references: GB:M83312; NID:gl553058
A/Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)
A/Note: this translation is not annotated in GenBank entry M83312, release 113.0
R/Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A/Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A/Reference number: A46515; MUID:93094586
A/Accession: A46515
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-287, 'LV' <GRI>
A/Cross-references: GB:M83312; NID:gl553058; PIDN:AAB08705.1; PID:gl553059; GB:M94126; N
A/Experimental source: BALB/C, liver
A/Note: sequence extracted from NCBI backbone (NCBI:P:120357)
C/Comment: For an alternative splice form, see PIR:A46515.
C/Comment: For an alternative splice form, see PIR:A46476.
C/Superfamily: CD27 antigen; NGF receptor repeat homology
C/Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 14.1%; Score 174; DB 2; Length 305;
Best Local Similarity 28.4%; Pred. No. 6.4e-06;
Matches 60; Conservative 30; Mismatches 91; Indels 30; Gaps 11;
QY 13 LVLELVGIVPSGIVGLPHLGRDREKRSVCPQGYIHPQNNISICTCKHKGTYLYNDC 72
Db 1 MVSPLRLCALW--GCLLTAVHLG----QCVTCSDKQYLH---DQCCDLCQPGSRLTSHC 51
QY 73 PPGQDTDCRECSGSTASENHLRHLCSCKRKGQVEISSCTVDRTVCGCRNQY 132
Db 52 TAL-ETQCTHPCDSGEFSAQWNRIRCHQHRCEPNOGLRVKKEGTAEISDTVCTCKEQ- 109
QY 133 RHYWSENLFOCFNCSLCLNG-TVHLSQEQKQNTVC-TCHAGFFLREN----ECVSCSNCK 186
Db 110 -HTSKDCEACAOHTPCIPGFGVNMEMATFTDVTCHPCVPVGFFSNQSLFEKYPWTSC 168
QY 187 -KSLCTKLCPLQIENYKGTEDSGTIVLLPL 216
Db 169 DKNLEVLQ-----KGT--SQTNVICGL 188

RESULT 14
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C/Species: variola minor virus
C/Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
R/Accession: D72175
R/Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Massung, R.F.; Lopan
submitted to GenBank, March 1998
A/Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A/Reference number: A72150
A/Accession: D72175
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-349 <SHC>
A/Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830759
A/Experimental source: strain Garcia-1966
C/Genetics:
A/Gene: G2R
C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 13.5%; Score 166.5; DB 2; Length 349;
Best Local Similarity 26.7%; Pred. No. 2.5e-05;
Matches 46; Conservative 19; Mismatches 64; Indels 43; Gaps 9;
QY 44 CPQGYIHPQNNISICTCKHKGTYLYNDCPGQDTCRECSGSTASENHLRHLCS 103
Db 32 CKDTEY----KRHLCCLSCLPPGTYASRLCDK-TNTQCTPCGSGTFTSRNHLPA 87
QY 104 -KCRKEMQVEISSCTVDRTVCGCRKNQYRHYWSENLFOCF-----NCSLCLNGTVHLS 157
Db 88 GRCNS--NQVETRSCTNTHNRICECSPGY-----CLLKSGSGCKACVSQT---- 131
QY 158 COEKQNTVCTCHAGFFLRENECVS---CSNC-----KKSLECTKLCPLQIEN 201
Db 132 -----KCGIGYGVSGHTSVGDVICSPCGFGTYVTVSVDKCEPVNN 174
RESULT 15
T28623
hypothetical protein G2R - variola major virus
C/Species: variola major virus
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C/Accession: T28623
R/Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au
Nature 366, 748-751, 1993
A/Title: Potential virulence determinants in terminal regions of variola smallpox vir
A/Reference number: 220488; MUID:94088747
A/Accession: T28623
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-348 <MAS>
A/Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A/Experimental source: strain Bangladesh 1975
C/Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 13.3%; Score 164; DB 2; Length 348;
Best Local Similarity 27.8%; Pred. No. 3.8e-05;
Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;
QY 44 CPQGYIHPQNNISICTCKHKGTYLYNDCPGQDTCRECSGSTASENHLRHLCS 103
Db 31 CKDTEY----KRHLCCLSCLPPGTYASRLCDK-TNTQCTPCGSGTFTSRNHLPA 86
QY 104 -KCRKEMQVEISSCTVDRTVCGCRKNQYRHYWSENLFOCF-----NCSLCLNGTVHLS 157
Db 87 GRCNS--NQVETRSCTNTHNRICECSPGY-----CLLKSGSGCKACVSQT---- 130
QY 158 COEKQNTVCTCHAGFFLRENECVS---CSNC 185
Db 131 -----KCGIGYGVSGHTSVGDVICSPC 152

Search completed: August 14, 2001, 05:37:34
Job time: 251 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 05:37:08 ; Search time 1190.68 seconds
(without alignments)
11094.045 Million cell updates/sec

Title: US-09-599-400A-1
Perfect score: 854
Sequence: 1 gactgagagccatagctgt:.....ggcgcagcagcaaatggg 854

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_ba3.*
- 4: gb_in1.*
- 5: gb_in2.*
- 6: gb_in3.*
- 7: gb_om.*
- 8: gb_ov.*
- 9: gb_pat1.*
- 10: gb_pat2.*
- 11: gb_ph.*
- 12: gb_pl1.*
- 13: gb_pl2.*
- 14: gb_pl3.*
- 15: gb_pl4.*
- 16: em_ba1.*
- 17: em_ba2.*
- 18: em_fun.*
- 19: em_htgo_hum.*
- 20: em_htgo_inv.*
- 21: em_htgo_rod.*
- 22: em_htg_hum1.*
- 23: em_htg_hum2.*
- 24: em_htg_hum3.*
- 25: em_htg_hum4.*
- 26: em_htg_hum5.*
- 27: em_htg_hum6.*
- 28: em_htg_hum7.*
- 29: em_htg_hum8.*
- 30: em_htg_inv1.*
- 31: em_htg_inv2.*
- 32: em_htg_other.*
- 33: em_htg_rod.*
- 34: em_hum1.*
- 35: em_hum2.*
- 36: em_hum3.*
- 37: em_hum4.*
- 38: em_hum5.*
- 39: em_hum6.*
- 40: em_hum7.*
- 41: em_in.*
- 42: em_om.*
- 43: em_or.*

- 44: em_ov.*
- 45: em_pat.*
- 46: em_ph.*
- 47: em_pl.*
- 48: em_rod.*
- 49: em_sts.*
- 50: em_sy.*
- 51: em_un.*
- 52: em_vi.*
- 53: gb_sts1.*
- 54: gb_sts2.*
- 55: gb_sts3.*
- 56: gb_sy.*
- 57: gb_un.*
- 58: gb_v1.*
- 59: gb_v12.*
- 60: gb_htg1.*
- 61: gb_htg2.*
- 62: gb_htg3.*
- 63: gb_htg4.*
- 64: gb_htg5.*
- 65: gb_htg6.*
- 66: gb_htg7.*
- 67: gb_htg8.*
- 68: gb_htg9.*
- 69: gb_htg10.*
- 70: gb_htg11.*
- 71: gb_htg12.*
- 72: gb_htg13.*
- 73: gb_htg14.*
- 74: gb_htg15.*
- 75: gb_htg16.*
- 76: gb_htg17.*
- 77: gb_htg18.*
- 78: gb_htg19.*
- 79: gb_htg20.*
- 80: gb_htg21.*
- 81: gb_htg22.*
- 82: gb_htg23.*
- 83: gb_htg24.*
- 84: gb_htg25.*
- 85: gb_pr1.*
- 86: gb_pr2.*
- 87: gb_pr3.*
- 88: gb_pr4.*
- 89: gb_pr5.*
- 90: gb_pr6.*
- 91: gb_pr7.*
- 92: gb_pr8.*
- 93: gb_pr9.*
- 94: gb_rod.*
- 95: gb_rod2.*
- 96: gb_in4.*
- 97: gb_pr10.*
- 98: gb_ba3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	676.6	79.2	2050	97	HUMTNFRP
2	676.6	79.2	2062	9	A21522
3	676.6	79.2	2062	10	I43805
4	676.6	79.2	2087	97	HUMTNFR
5	676.6	79.2	2111	9	A26412
6	676.6	79.2	2111	97	HUMTNFRB
7	676.6	79.2	2161	9	AR096330
8	676.6	79.2	2161	93	HSTNFR1A
					M60275 Human tumor
					A21522 TNF alpha g
					I43805 Sequence 24
					M33294 Human tumor
					A26412 cDNA for (5
					M58286 Homo sapien
					AK096330 Sequence
					X55313 H.sapiens T

Db 850 AATGATATCGCT 860

RESULT 2

A21522 2062 bp mRNA PAT 26-JUL-1994

LOCUS TNF alpha gene.

DEFINITION

ACCESSION A21522

VERSION

A21522.1 GI:579599

KEYWORDS

human.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 2062)

Patent: GB 2246569-A 1 05-FEB-1992;

Location/Qualifiers

1..2062

/organism="Homo sapiens"

/db_xref="taxon:9606"

155..1522

/gene="TNF alpha gene"

155..1522

/gene="TNF alpha gene"

/codon_start=1

/protein_id="CAA01558.1"

/db_xref="GI:579600"

/db_xref="SWISS-PROT:P19438"

/translation="MGLSTVPDLLPLVLELLVGYPSGVIGLVPHLGDREKRSVC

PQKYIHPQNNISICCTKDKGTLYNDQPGQDQDCRECSGFTASNHRLHCLSC

SKRKEMQVSEISCTVDRDTCGCRKQYRHWSENLFQCPNCSLICLNGTVHLSCQE

KQNVCTCHAGFFLEENSCVSNCKKSLKCLPQLENVKGTEDSYTVLLPLVI

FGCLLSLLILGLMRTYQWRKSKLSIVGKSTPEKGELEGITKPLAPNPSPST

PGFTLLSPVPSYTSSTYTPGDCPNFAAPREVAPPYQGGADPILATLASDPI

PNLQKWDASHKPOSLLDDPATLYAVVNNPPLRWFKEFVRRLGSLDHEIDRLQON

GRCLREAOYSMLATWRRRTPREATLELLGLRVLDMDLLGLCLEDIEALCGPAALPPA

PSLLR"

BASE COUNT 429 a 617 c 573 g 443 t

ORIGIN

Query Match 79.2%; Score 676.6; DB 9; Length 2062;

Best Local Similarity 95.3%; Pred. No. 4.2e-178;

Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 gagtgaagagccatagctgtctggcattggcctctccaccgtgcctgacctgctgtgcc 60

Db 130 GAGTGAGAGGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGCCTGACCTGCTGTGCC 189

QY 61 gctggtctctggagctgttggtgggaatataccctcagggttatgtgacctgtgcc 120

Db 190 GCTGGTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 249

QY 121 tcacctaggagcagagagagagatagtggtgtcccaaggaaataatataccacc 180

Db 250 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATAATATATCCACCC 309

QY 181 tcaaaataattcgattgtgtaccagtgcacaaaggaaacctactgtgacaatgactg 240

Db 310 TCAAAATAATTTCGATTTCGTTACCAAGTGCCACAAAGAACCTACTTGTACAAATGACTG 369

QY 241 tccagggccgggacgagatcacgactgcaggagtgtgagagcggtccttaccgcttc 300

Db 370 TCCAGGCGGGGACGAGTACGAGCTGACGGAGTGTGAGAGCGGCTCTTCCACCGCTTC 429

QY 301 aaaaaaccacctcagacactgctcagctgctcctaattgccaaaggaatgggtcaggt 360

Db 430 AGAAAACCAACCTCAGACACTGCTCTAGCTGCTCCAAATGCCGAAGAAATGGTCAGGT 489

QY 361 ggagatctctctgacagtgagcgggacacccgtgtgtggctgcaggaagaacagta 420

Db 490 GGAGATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAGAACCACTA 549

QY 421 ccgcatatttgagtgagaaacacccctttccagtgcttcaattgcagcctctgcctcaatgg 480

Db 550 CCGCATATTGAGTGAACAAACCTTTTCCAGTGTCTCAATTGCAGCCTCTGCTCAATGG 609

QY 481 gacgtgacactctctctccaggagagaaacacacacacacacacacacacacacacacac 540

Db 610 GACCGTGACCTCTCTCCGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGACAGTTT 669

QY 541 ctttctaagagaaac 600

Db 670 CTTTCTAAGAGAAACACGAGTGTCTCTGTAGTAACCTGTAAAGAAACCTTGGAGTGAC 729

QY 601 gaattgtgctaccac 660

Db 730 GAAGTTGTGCTACCCACAGATTGAGAAATGTAAGGACACTGAGGACTCAGGACACACAGT 789

QY 661 gctgtgcccctctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 720

Db 790 GCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849

QY 721 ttgtttttgtt 731

Db 850 AATGATATCGCT 860

RESULT 3

I43805 2062 bp DNA PAT 07-OCT-1997

LOCUS

DEFINITION Sequence 24 from patent US 5633145.

ACCESSION I43805

VERSION I43805.1 GI:2468903

KEYWORDS

Unknown.

SOURCE

ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 2062)

AUTHORS Feldmann, M., Gray, P.W., Turner, M.J.C. and Brennan, F.M.

TITLE TNF alpha receptor-derived binding protein

JOURNAL Patent: US 5633145-A 24 27-MAY-1997;

FEATURES

Location/Qualifiers

1..2062

source

BASE COUNT 429 a 617 c 573 g 443 t

ORIGIN

Query Match 79.2%; Score 676.6; DB 10; Length 2062;

Best Local Similarity 95.3%; Pred. No. 4.2e-178;

Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 gagtgaagagccatagctgtctggcattggcctctccaccgtgcctgacctgctgtgcc 60

Db 130 GAGTGAGAGGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGCCTGACCTGCTGTGCC 189

QY 61 gctggtctctggagctgttggtgggaatataccctcagggttatgtgacctgtgcc 120

Db 190 GCTGGTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 249

QY 121 tcacctaggagcagagagagagatagtggtgtcccaaggaaataatataccacc 180

Db 250 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATAATATATCCACCC 309

QY 181 tcaaaataattcgattgtgtaccagtgcacaaaggaaacctactgtgacaatgactg 240

Db 310 TCAAAATAATTTCGATTTCGTTACCAAGTGCCACAAAGAACCTACTTGTACAAATGACTG 369

QY 241 tccagggccgggacgagatcacgactgcaggagtgtgagagcggtccttaccgcttc 300

Db 370 TCCAGGCGGGGACGAGTACGAGCTGACGGAGTGTGAGAGCGGCTCTTCCACCGCTTC 429

QY 301 aaaaaaccacctcagacactgctcagctgctcctaattgccaaaggaatgggtcaggt 360


```

Db 430 AGAAACACCTCAGACACTGCCTCAGCTGCTCCAAATGCCAAAGGAAATGGGTCAGGT 489
Qy 361 ggagatctcttttgcacagtgagaccggagacacggtgtgtgctgcaggaagaaccagta 420
Db 490 GGAGATCTCTTCTTGTGCACAGTGGACCGGGACACCGCTGTGTGGCTGCAGGAAGAACAGTA 549
Qy 421 ccgcatattggagtgaaacaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 550 CCGCATATTGGAGTGAAACACCTTTTCCAGTGTCTCAATTCAGCCCTCTGCCTCAATGG 609
Qy 481 gacgtgcacctctcctccagggagaaacagacacacccgtgtgcacctgccatgccaggttt 540
Db 610 GACCGTGACCTCTCCCTGCCAGGAAACACACACCCGTGTGCACCTGCCATGCAGGTTT 569
Qy 541 ctttetaagaaacagtggtgtctctctgtagtaactgtgaagaaacccctggagtgac 600
Db 670 CTTTCTAAGAAACAGAGTGTCTCCTGTAGTAACCTGTAAGAAAGCCCTGGAGTGCAC 729
Qy 601 gaagtgtgctacccacagattgagaattgtaaggagcactgaggaactcaggcaccacagt 660
Db 730 GAAGTTGTGCTACCCACAGATGGAATGTTAAGGGCACTGAGGACTCAGGCACACAGT 789
Qy 661 gctgtgcccctggtgtcctcctgagccttttccacagtcataagcagttttttgtt 720
Db 790 GCTGTGCCCTGTGTCATTTCTTGTGCTTTCCTTTTATCCCTCCCTTCATTCAGTGT 849
Qy 721 ttgtttttgtt 731
Db 850 AATGTATCGCT 860

RESULT 4
HUMTNFR 2087 bp mRNA PRI 10-NOV-1993
LOCUS Human tumor necrosis factor receptor mRNA, complete cds.
DEFINITION M33294
ACCESSION M33294
VERSION M33294.1 GI:339744
KEYWORDS cell surface receptor; tumor necrosis factor receptor.
SOURCE Human placenta, cdNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2087)
AUTHORS Schall,T.J., Lewis,M., Koller,K.J., Lee,A.L., Rice,G.C., Wong,G.H.,
Gatanaga,T., Granger,G.A., Lentz,R., Raab,H., Kohr,W.J. and
Goeddel,D.V.
TITLE Molecular cloning and expression of a receptor for human tumor
necrosis factor
JOURNAL Cell 61, 361-370 (1990)
MEDLINE 90235285
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by T.Schall, 26-MAR-1990.
FEATURES
source Location/Qualifiers
1..2087
/organism="Homo sapiens"
/db_xref="taxon:9606"
182..1549
/note="tumor necrosis factor receptor"
/codon_start=1
/protein_id="AA03210.1"
/db_xref="GI:339745"
/translaton="MGLSTVDPDLLPLVLELLVGVPSGVIGLVPHLGDREKRDSVC
POKGYIHPQNSICCTKCHKGTVLYNDPGQDTCRECEGSFTASENHLRLCLSC
SKRKEGQVEIISCTVDVDRVCGCRKNQYRHYWSENLFOCFNCLINGTVHLSCOE
KONTVCTHAGFFLRENECVSCNKKSLCTKLCPLQIENVKGTESGTVLLPLVI
FGLGLLSLFIQLMRYQWKSLSIVCGKSLPEKELEGITTPAPNPSPST
PGFTPLQWEDSAHPQSDLTDPATLYAVVNPFRWKEFVRRLGSLDHEIDRLQNL
PCLRLAQYSLMATWRRTRPRATLELLGLVRLMDLLGLCLEDIEALCGPAALPPA
PSLLR"
BASE COUNT 433 a 624 c 581 g 449 t
ORIGIN

```

```

Query Match 79.2%; Score 676.6; DB 97; Length 2087;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gagtgaagagccatagctgtctggaatggccctctccacgtgctgacgtgctgctgccc 60
Db 157 GAGTGAGAGGCCATAGCTGTCTGGCATGGGCCCTCCACCGTGCCTGACCTGTGTGCC 216
Qy 61 gctggtgctccctggagctgttgggtggaataataccctcaggggttattgagctggtccc 120
Db 217 GCTGTGCTCTCTGGAGCTGTGTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 276
Qy 121 tcacctaggggagagggagagagatagtggtgtcccccaaggagaaataatatcacccc 180
Db 277 TCACCTAGGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATATCCACCC 336
Qy 181 tcaaaataattgattgtgtaccgaagtgccacaagaacctaactgttacaatgactg 240
Db 337 TCAAAATAATTGATTGTGTGTACCAAGTGCCACAAGGAACCTACTTGTACAAATGACTG 396
Qy 241 tccaggccggggcaggatcacgactgcaggagtgagagcggtcctctcaccgcttc 300
Db 397 TCCAGGCCCGGGCAGGATACGACTGCAGGGAGTGTGAGAGCGGCTCTCTACCGCTTC 456
Qy 301 agaaaaccacctcagacactgcctcagctgtctccaaatgccgaaagaaaatgggtcaggt 360
Db 457 AGAAAACCACTCAGACACTGCCTCAGCTGCTCCAAATGCCAAAGGAAATGGTCAAGT 516
Qy 361 ggagatctctttgcacagtgagccgggacacccgtgtgtgctgcaggagaagaccagta 420
Db 517 GGAGATCTCTTCTTGCACAGTGGACCGGACACCGGTGTGTGGCTGCAGGAAGAACAGTA 576
Qy 421 ccgcatattgagtgaaacaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 577 CCGCATATTGGAGTGAAACCTTTTCCAGTGTCTCAATTGCAGGCTCTGCCCTCAATGG 636
Qy 481 gacctgtcacctctctcctgcaggagaaacagaaacacacacccgtgtgcacctgcaggttt 540
Db 637 GACCGTGCACCTCTCTCTGCCAGGAGAAACAGAACACCGGTGTGCACCTGCCATGCAGGTTT 696
Qy 541 ctttctaagagaaaacagagtgctctcctctgtagtaactgtaagaaaagcctggagtgac 600
Db 697 CTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 756
Qy 601 gaagtgtcctcaccacagattgagaatgtaaggacactgaggaactcaggcaccacagt 660
Db 757 GAAGTTGCTCTACCCACATTTGAGAAATGTAAGGCACCTGAGGACTCAGGCACACAGT 816
Qy 661 gctgttgcccctgggttcctcctgagccttttccacagtgcataagcaggtttttttgtt 720
Db 817 GCTGTGCCCCCTGGTCATTTCTTTTGTGCTTTTGTGCTTTTATCCCTCTCTCTCATTTGTTT 876
Qy 721 ttgtttttgtt 731
Db 877 AATGTATCGCT 887

RESULT 5
A26412 2111 bp DNA PAT 26-APR-1995
LOCUS CDNA for (55kD TNF-BP) tumor necrosis factor binding protein from
DEFINITION patent EP04117563.
ACCESSION A26412
VERSION A26412.1 GI:904968
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Brockhaus,M., Dambic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
Schlaeger,E.J.
TITLE TNF-binding proteins

```

JOURNAL Patent: EP 0417563-A 24 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
FEATURES Location/Qualifiers
source 1..2111
/organism="synthetic construct"
/db_xref="taxon:32630"
187..1554
/codon_start=1
/transl_table=11
/product="55 kd TNF-Bp"
/protein_id="CAA01805.1"
/db_xref="GI:904969"
/translation="MGLSTVDPDLLPLVLLLELVGIVPSGIVGLPHGLDRKRSVC
POGKIIPQNNISICTKHKGTLYLNDPCPGQDTCRECSGFTASENHLRLCLSC
SKCRKEMGOVEISSCTVDRDTCGRKNOYRHYSENLCNCTVHLSCOE
KONTVCTCHAGFFLENECVSCNCKSLCTKLPQIENVKGTEDSGTIVLLPLVI
FFGLCLSLFGLMYRYQRKSKLSYIVCGKSTPEKEGELEGTTPKLPAPNPSFPT
PGFTPTLGFSPVPSSTFTSSSTYPGDCPNFAAPREVAPYQGADPILATLASDPI
PNPLOWEDSAHKQSLDTPDPAIYAVVENVPLRWKFVRRLGLSDHEIDRLQLN
GRCLREAOYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPA
PSLLR"
BASE COUNT 445 a 629 c 587 g 450 t
ORIGIN
Query Match 79.2%; Score 676.6; DB 9; Length 2111;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 gagttagagccatagctgtctgcatggccctctccacgtgctgacctgctgctgc 60
DB 162 GAGTGAGAGCCATAGCTGCTGGCATGGGCTCTCCACCGTGCCTGACCTGCTGCC 221
QY 61 gctgtgctcctggagcctgttgaggaaataaccctcaggggttattggactgctcc 120
DB 222 GCTGTGCTCTCGAGCTGTTGGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 281
QY 121 tcacctaggagcagagagagatagtggtgtcccccaggaataatatccaccc 180
DB 282 TCACCTAGGGACAGGAGAGAGATAGTGTGTGCCCAAGGAANAATATATCCACCC 341
QY 181 tcaaaataattgattgtgtaccagtgccacaaagaaacctactgtacaatgactg 240
DB 342 TCAAAATAATTGATTGTGTGTACCAAGTGCCACAAAGAACTACTTGTACAATGACTG 401
QY 241 tccagggccgggagagatacagactcagggagtgtagcggtgctcctcaccgcttc 300
DB 402 TCCAGGCCCGGGCAGGATACGAGTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTC 461
QY 301 agaaaaccacctcagacactgctcagctgtctccaaatgccgaagaaatgggtcaggt 360
DB 462 AGAAAACCACCTCAGACACTGCTCAGCTGCTCCAAATGCCGAAGAAATGGGTGAGT 521
QY 361 gagatctctcttcacagtgagcgggacacccgtgtgtgctgtaggaagaacagta 420
DB 522 GGAGATCTCTTTCACAGTAGTGACGGGACACCGTGTGTGCTGCAGGAGAACAGTA 581
QY 421 ccggcattattgagtgaaaccttttccagtgcttcaattgacgctctgctcctcaatgg 480
DB 582 CGGCATATTGAGTGAAACCTTTTCCAGTGTCTCAATTGCAGCCTCTGCCTCAATGG 641
QY 481 gacctgacctctcctgccagagaaacacagacctgtgacctgcatgcatgaggttt 540
DB 642 GACCCGTGACCTCTCTCGCAGGAGAAACAGAACACCGTGTGCACCTGCGCATGCAAGTTT 701
QY 541 ctttctaagagaaacagatgtgtctctgtagtactgaactaagaaagcctgagtgac 600
DB 702 CTTTCTAAGAGAAAAGAGTGTGTCTCTGTAGTAAGTGTAAAGGAAAGCTGGAGTGCAC 761
QY 601 gaagttgtcctaccctcagattgagaatgttaaggscactgaggtcctcagggcaccag 660
DB 762 GAAGTTGTGCTACCCAGATGAGAAATGTTAAGGCACTGAGGACTCAGGCACACAGT 821

QY 661 gctgttgccctggttcctccctgagccttttccacagtgcataagcagctgtttttgtt 720
DB 822 GCTGTGCCCTCGTCAATTTCTTGTGCTTTTATGCTCTTATFCCCTCTCTTCATTGGTTT 881
QY 721 ttgtttttgtt 731
DB 882 AATGTATCGCT 892
RESULT 6
LOCUS HUMTNFRB 2111 bp mRNA PRI 03-AUG-1993
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
ACCESSION M58286.1 M33480
VERSION M58286.1 GI:339753
KEYWORDS tumor necrosis factor receptor.
SOURCE Human cell line HL60, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Loetscher,H., Pan,Y.-C.E., Lahm,H.-W., Gentz,R., Brockhaus,M.,
Tabuchi,H. and Lesslauer,W.
TITLE Molecular cloning and expression of the human 55 kd tumor necrosis
factor receptor
JOURNAL Cell 61, 351-359 (1990)
MEDLINE 90235284
FEATURES Location/Qualifiers
source 1..2111
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HL60"
187..273
sig_peptide
/gene="TNF receptor"
/product="tumor necrosis factor receptor"
187..1554
CDS
/gene="TNF receptor"
/notes="55 kDa"
/codon_start=1
/product="tumor necrosis factor receptor"
/protein_id="AAA36753.1"
/db_xref="GI:339754"
/translation="MGLSTVDPDLLPLVLLLELVGIVPSGIVGLPHGLDRKRSVC
POGKIIPQNNISICTKHKGTLYLNDPCPGQDTCRECSGFTASENHLRLCLSC
SKCRKEMGOVEISSCTVDRDTCGRKNOYRHYSENLCNCTVHLSCOE
KONTVCTCHAGFFLENECVSCNCKSLCTKLPQIENVKGTEDSGTIVLLPLVI
FFGLCLSLFGLMYRYQRKSKLSYIVCGKSTPEKEGELEGTTPKLPAPNPSFPT
PNPLOWEDSAHKQSLDTPDPAIYAVVENVPLRWKFVRRLGLSDHEIDRLQLN
GRCLREAOYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLDEIEEALCGPAALPPA
PSLLR"
gene 187..1554
/gene="TNF receptor"
mat_peptide 274..1551
/gene="TNF receptor"
/product="tumor necrosis factor receptor"
BASE COUNT 445 a 629 c 587 g 450 t
ORIGIN
Query Match 79.2%; Score 676.6; DB 97; Length 2111;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 gagttagagccatagctgtgcatggccctctccacgtgctgacctgctgctgc 60
DB 162 GAGTGAGAGCCATAGCTGCTGGCATGGGCTCTCCACCGTGCCTGACCTGCTGCC 221
QY 61 gctgtgctcctggagcctgttgaggaaataaccctcaggggttattggactgctcc 120
DB 222 GCTGTGCTCTCGAGCTGTTGGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 281
QY 121 tcacctaggagcagagagagatagtggtgtcccccaggaataatatccaccc 180

```

Db 282 TCACCTAGGGACAGGAGAGAGATAGTGTGTCCTCCCAAGGAATAATATATCACCC 341
Qy 181 tcaaaataattcgtatttctgtaccaaagtcacaaagaaacactactgtacaatgactg 240
Db 342 TCAAAATAATTGGAFTTCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTG 401
Qy 241 tccaggccggggcaggatagcaggactcaggagtgtagagcggcctcctccaccgttc 300
Db 402 TCCAGGCCGGGGCAGGATACGAGTACGAGGAGTGTGAGAGCGGCTCCTTCACCGCTTC 461
Qy 301 agaaaacacactcagacactccctcagctgtccaaatgccgaaggaatgggtcaggt 360
Db 462 AGAAACACACCTCAGACACTGCTCAGCTGTCTCAAAATGCCGAAAGGAATGGTCAGGT 521
Qy 361 ggagatctctctgtcacagtgagcgggagcacccgtgtgtggtgcaggaaagaaacagta 420
Db 522 GGAGATCTCTTGTGCACAGTGGACCGGGACACCGTGTGTGCTGCAGGAAGAACAGTA 581
Qy 421 ccggcattatggagtgaaaacctttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 582 CCGGCAATTATTGGAGTGAACCTTTTCCAGTGTCTCAATTCAGCCCTCTGCCTCAATGG 641
Qy 481 gaccgtcacctctcctccaggagaaacagaaacacccgtgtgcacctgccatgcagggtt 540
Db 642 GACCGTGACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTT 701
Qy 541 ctcttaagaaaaacagtggtctcctctgtagtaactgtgaagaaagcctgagtgac 600
Db 702 CTTTCTAGAGAAACAGTAGTGTCTCTGTAGTAACGTGTAAGAAAGCCCTGAGGTGAC 761
Qy 601 gaagttgctacccagatgtagaatgttaagggcactgaggactcaggcaccacagt 660
Db 762 GAAGTTGTGCTACCCAGATTGAGAAATGTTAAGGGCACTGAGGACTCAGGCACACAGT 821
Qy 661 gctgtgcccctggtctccctcagccttttccagtgcttaagcagtgataagcagttttt 720
Db 822 GCTGTGCCCCGTGTCATTTCTTGTGCTTTTGCCTTTTATCCCTCCTCTTCATTTGGTT 881
Qy 721 ttgtttgtt 731
Db 882 AATGATCGCT 892

RESULT 7
AR096330 2161 bp DNA PAT 08-SEP-2000
LOCUS AR096330 Sequence 1 from patent US 6007995.
DEFINITION AR096330
ACCESSION AR096330
VERSION AR096330.1 GI:10025045
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2161)
AUTHORS Baker,B.F. and Cowser,L.M.
TITLE Antisense inhibition of TNFR1 expression
JOURNAL Patent: US 6007995-A 1 28-DEC-1999;
FEATURES
    Location/Qualifiers
        source
            1..2161
                /organism="unknown"
BASE COUNT 459 a 642 c 456 t
ORIGIN

Query Match 79.2%; Score 676.6; DB 9; Length 2161;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gagtgaaggccatagctgtctggcatgggcccctccaccctgcctgacctgctgtgcc 60
Db 231 GAGTGAGAGGCCATAGTGTGTGGCATGGGCTCTCCACCGCTGCTGCTGCTGCTGCC 290

```

```

Qy 61 gctgtgtcctcctggagctgttgggtgggaatataccctcctcaagggtttattggactggtccc 120
Db 291 GCTGTGTCCTCTGGAGCTGTGTGGTGGAAATATACCCCTCAGGGGTTATTGGACTGGTCCC 350
Qy 121 tcaacctaggagcagaggagaaagagatagtggtgtcccccaaggaaataatatcacccc 180
Db 351 TCACCTAGGGACAGGAGGAAGAGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 410
Qy 181 tcaaaaataattcgtatttctgtaccaaagtcacaaagaaacactactgttacaatgactg 240
Db 411 TCAAAATAATTGGAFTTCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTG 470
Qy 241 tccaggccggggcaggatagcaggactcaggagtgtagagcggcctcctccaccgttc 300
Db 471 TCCAGGCCGGGGCAGGATACGAGTACGAGGAGTGTGAGAGCGGCTCCTTCACCGCTTC 530
Qy 301 agaaaacacactcagacactccctcagctgtccaaatgccgaaggaatgggtcaggt 360
Db 531 AGAAACACACCTCAGACACTGCTCAGCTGTCTCAAAATGCCGAAAGGAATGGTCAGGT 590
Qy 361 ggagatctctctgtcacagtgagcgggagcacccgtgtgtggtgcaggaaagaaacagta 420
Db 591 GGAGATCTCTTGTGCACAGTGGACCGGGACACCGTGTGTGCTGCAGGAAGAACAGTA 650
Qy 421 ccggcattatggagtgaaaacctttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 651 CCGGCAATTATTGGAGTGAACCTTTTCCAGTGTCTCAATTCAGCCCTCTGCCTCAATGG 710
Qy 481 gaccgtcacctctcctccaggagaaacagaaacacccgtgtgcacctgccatgcagggtt 540
Db 711 GACCGTGACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTT 770
Qy 541 ctcttaagaaaaacagtggtctcctcctgtagtaactgtgaagaaagcctgagtgac 600
Db 771 CTTTCTAGAGAAACAGTAGTGTCTCTGTAGTAACGTGTAAGAAAGCCCTGAGGTGAC 830
Qy 601 gaagttgctacccagatgtagaatgttaagggcactgaggactcaggcaccacagt 660
Db 831 GAAGTTGTGCTACCCAGATTGAGAAATGTTAAGGGCACTGAGGACTCAGGCACACAGT 890
Qy 661 gctgtgcccctggtctccctcagccttttccagtgcttaagcagtgataagcagttttt 720
Db 891 GCTGTGCCCCGTGTCATTTCTTGTGCTTTTGCCTTTTATCCCTCCTCTTCATTTGGTT 950
Qy 721 ttgtttgtt 731
Db 951 AATGATCGCT 961

RESULT 8
HSTNFR1A 2161 bp mRNA PRI 18-JAN-1993
LOCUS HSTNFR1A H.sapiens TNF-R mRNA for tumor necrosis factor receptor type 1.
DEFINITION X55313
ACCESSION X55313.1 GI:37223
VERSION X55313.1
KEYWORDS TNF-R gene; tumor necrosis factor receptor 1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2161)
AUTHORS Nopha,Y., Kemper,O., Brakebusch,C., Englemann,H., Zwang,R.,
Aderka,D., Holtmann,H. and Wallach,D.
TITLE Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
for the type I TNF-R, cloned using amino acid sequence data of its
soluble form, encodes both the cell surface and a soluble form of
the receptor
JOURNAL EMBO J 9 (10), 3269-3278 (1990)
MEDLINE 91006021
FEATURES
    Location/Qualifiers
        1..2161
            /organism="Homo sapiens"
            /db_xref="taxon:9606"

```

```
gene          256..2161
              /gene="TNF-R"
CDS            256..1623
              /gene="TNF-R"
              /codon_start=1
              /product="tumor necrosis factor receptor type 1"
              /protein_id="CAA39021.1"
              /db_xref="GI:37224"
              /db_xref="SWISS-PROT:P19438"
              /translation="MGLSTVPDLPLPLVLELLVGIYPSGVIGLVPHLGDREKRDVSC
POGKYIHPONNSICCTCKHKGYLYNDPCPGQDTCRECEGSFTASENHLRHLCS
SKCRKEMQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGVHLSCOE
KQNTVCTCHAGFFLRNECVSCNCKSLECTKICLPQIENYKGFEDSGTIVLLPLVI
FPGCLLSLLFLIGLMYRQWKSILYSIVCGKSTPEKEGELEGTTPKPLANPSFPT
PFQTLTGFSVPSTFTSSSYTPGDCNFAAPREVAIPPYQADPIATALASDP1
PNPLQKWEDSAHKPQSLDTPDPAIYAVVENVPPLRWKEFVRRLGLSDHEIDRLQLN
GRCLREAQYSMLATWRRRTPREATLELLGRVLRMDLLGLCLEDEALCGPAALPPA
PSLLR"
repeat_region 385..504
repeat_region 505..633
repeat_region 634..756
repeat_region 757..857
polyA_signal  2145..2150
              /gene="TNF-R"
              /note="putative"
              /db_xref="GI:37224"
              /db_xref="SWISS-PROT:P19438"
              /translation="MGLSTVPDLPLPLVLELLVGIYPSGVIGLVPHLGDREKRDVSC
POGKYIHPONNSICCTCKHKGYLYNDPCPGQDTCRECEGSFTASENHLRHLCS
SKCRKEMQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGVHLSCOE
KQNTVCTCHAGFFLRNECVSCNCKSLECTKICLPQIENYKGFEDSGTIVLLPLVI
FPGCLLSLLFLIGLMYRQWKSILYSIVCGKSTPEKEGELEGTTPKPLANPSFPT
PFQTLTGFSVPSTFTSSSYTPGDCNFAAPREVAIPPYQADPIATALASDP1
PNPLQKWEDSAHKPQSLDTPDPAIYAVVENVPPLRWKEFVRRLGLSDHEIDRLQLN
GRCLREAQYSMLATWRRRTPREATLELLGRVLRMDLLGLCLEDEALCGPAALPPA
PSLLR"
polyA_site    2161
BASE COUNT   459 a 642 c 604 g 456 t
ORIGIN
Query Match      79.2%; Score 676.6; DB 93; Length 2161;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gagtggagggccatagctgtctggcatggcctctccaccgtgcctgacctgctgtgcc 60
Db 231 GAGTGAGAGGCCATAGCTGCTGGCATGGCGCTCTCCACCGCTGCCTGACCTGCTGTGCC 290

Qy 61 gctgtgtcctcaggagctgtgtgggaataataacctcagggttattggaactgtgcc 120
Db 291 GCTGTGCTCCTCGAGCTGTTGGTGGGAATATACCCCTCAGGGGTATTGGAGTGGTCCC 350

Qy 121 tcacctagggagcaggagagagatagtggtgtcccccaaggaaataatcccccc 180
Db 351 TCACCTAGGGACAGGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCC 410

Qy 181 tcaaaataattcgtgtaccgaagtgcacaaaggaaacctacttgtacaatgactg 240
Db 411 TCAAAATAATTCTGATTGCTGTACCAAGTCCACAAAGAACCTACTTGTACAATGACTG 470

Qy 241 tcacggccggggcaggatacaggactgcaggagtgtagagcgctctccacgcttc 300
Db 471 TCCAGGCCCGGGCAGGATACGAGCTCAGGGAGTGTGAGAGCGGCTCTTACCCGCTTC 530

Qy 301 agaaaaaacacctcagacactgctcagctgtctccaaatgcccgaaggaaatgggtcaggt 360
Db 531 AGAAAAACCACTCAGACACTGCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAAGT 590

Qy 361 ggagatctcttgcacagtgagccgggacaccgtgtgtgctgcaggaagaacagta 420
Db 591 GGAGATCTCTTCTGCACAGTGGACCGGACACCGGTGTGTGCTGCAGGAAGAACCAGTA 650

Qy 421 ccggcattattgagtgaataaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 651 CCGGCATTTATGGAGTGAAACCTTTTCCAGTGCTCAATTGCAGGCTCTGCCTCAATGG 710

Qy 481 gaccctgcacctctcctgccaggagaaacagaccgtgtgtgcacctgccaatgagttt 540
Db 711 GACCCGTGCACTCTCTCTGCCAGGAGAAACAGAACACCGGTGTGCACCTGCATGCAGGTTT 770

Qy 541 ctttctaagagaaaacagagtggtgtctctctgtagttaactgtaagaaaagcctggagtgcac 600
|||||
```

```
-Db 771 CTTTCTAAGAGAAAACGAGTGTCTCCTCTAGTAACGTGAAGAAAAGCCTGGAGTGAC 830
Qy 601 gaagtgtgctaccaccagattgagaatttaagggcagctgagactcagaccacagct 660
|||||
Db 831 GAAGTTGTGCTACCCAGATGAGATGTTAAGGGCACTCAGGACATCAGGACACACAGT 890

Qy 661 gctgtgtcctcaggagctgtgtccctcagcctttttcacagtgcataagcagttttttgtt 720
|||||
Db 891 GCTGTGCTCCTCGAGCTGTTGGTGGGAATATACCCCTCAGGGGTATTGGAGTGGTCCC 950

Qy 721 ttgttttgttt 731
|||||
Db 951 AATGTATCGCT 961

RESULT 9
LOCUS A43873 2175 bp DNA PAT 06-MAR-1997
DEFINITION Sequence 1 from Patent EP0657536.
ACCESSION A43873
VERSION A43873.1 GI:2299022
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2175)
AUTHORS Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
TITLE Proteases capable of shedding the soluble TNF-receptor and TNF-R
derived peptides and antibodies against the proteases inhibiting
the shedding
JOURNAL Patent: EP 0657536-A 1 14-JUN-1995;
YEDA RES & DEV (IL)
COMMENT Other publication ZA 9407962 951121
Other publication JP 7194376 950801
Other publication AU 7574294 950504
Other publication CA 2133872 950413.
FEATURES
source 1..2175
/organism="unidentified"
/db_xref="taxon:32644"
256..1623
/note="unnamed protein product"
/codon_start=1
/protein_id="CAA02771.1"
/db_xref="GI:2299023"
/translation="MGLSTVPDLPLVLELLVGIYPSGVIGLVPHLGDREKRDVSC
POGKYIHPONNSICCTCKHKGYLYNDPCPGQDTCRECEGSFTASENHLRHLCS
SKCRKEMQVEISSCTVDRTVCGCRKNQYRHYWSENLFQCFNCSLCLNGVHLSCOE
KQNTVCTCHAGFFLRNECVSCNCKSLECTKICLPQIENYKGFEDSGTIVLLPLVI
FPGCLLSLLFLIGLMYRQWKSILYSIVCGKSTPEKEGELEGTTPKPLANPSFPT
PFQTLTGFSVPSTFTSSSYTPGDCNFAAPREVAIPPYQADPIATALASDP1
PNPLQKWEDSAHKPQSLDTPDPAIYAVVENVPPLRWKEFVRRLGLSDHEIDRLQLN
GRCLREAQYSMLATWRRRTPREATLELLGRVLRMDLLGLCLEDEALCGPAALPPA
PSLLR"
BASE COUNT 474 a 641 c 604 g 456 t
ORIGIN
Query Match 79.2%; Score 676.6; DB 9; Length 2175;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gagtggagggccatagctgtgtggcatggcctcaccacgtgcctgacctgctgtgcc 60
Db 231 GAGTGAGAGGCCATAGCTGCTGGCATGGCGCTCTCCACCGCTGCCTGACCTGCTGTGCC 290

Qy 61 gctgtgtcctcaggagctgtgtgggaataataacctcagggttattggaactgtgcc 120
Db 291 GCTGTGCTCCTCGAGCTGTTGGTGGGAATATACCCCTCAGGGGTATTGGAGTGGTCCC 350

Qy 121 tcacctagggagcaggagagagatagtggtgtcccccaaggaaataatcccccc 180
Db 351 TCACCTAGGGACAGGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCC 410

Qy 181 tcaaaataattcgtgtaccgaagtgcacaaaggaaacctacttgtacaatgactg 240
Db 411 TCAAAATAATTCTGATTGCTGTACCAAGTCCACAAAGAACCTACTTGTACAATGACTG 470

Qy 241 tcacggccggggcaggatacaggactgcaggagtgtagagcgctctccacgcttc 300
Db 471 TCCAGGCCCGGGCAGGATACGAGCTCAGGGAGTGTGAGAGCGGCTCTTACCCGCTTC 530

Qy 301 agaaaaaacacctcagacactgctcagctgtctccaaatgcccgaaggaaatgggtcaggt 360
Db 531 AGAAAAACCACTCAGACACTGCTCAGCTGCTCCAAATGCCGAAAGGAAATGGGTCAAGT 590

Qy 361 ggagatctcttgcacagtgagccgggacaccgtgtgtgctgcaggaagaacagta 420
Db 591 GGAGATCTCTTCTGCACAGTGGACCGGACACCGGTGTGTGCTGCAGGAAGAACCAGTA 650

Qy 421 ccggcattattgagtgaataaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 651 CCGGCATTTATGGAGTGAAACCTTTTCCAGTGCTCAATTGCAGGCTCTGCCTCAATGG 710

Qy 481 gaccctgcacctctcctgccaggagaaacagaccgtgtgtgcacctgccaatgagttt 540
Db 711 GACCCGTGCACTCTCTCTGCCAGGAGAAACAGAACACCGGTGTGCACCTGCATGCAGGTTT 770

Qy 541 ctttctaagagaaaacagagtggtgtctctctgtagttaactgtaagaaaagcctggagtgcac 600
|||||
```

Qy	181	tcaaaa	taattcgattgctgtacc	aaagtcccaaaaggaaccta	cttgttacaatgacgtg	240	
Db	411	TCAAATAA	TTTGGTGTACCAAGT	GCCCAAAAGGAACCTACT	TGTGTACAATGACTG	470	
Qy	241	tcaaggcc	ggggcagagatacag	gaactgcaggagtgatg	aaagcggctccttcaacgccttc	300	
Db	471	TCCAGG	CCGGGCGAGGATAC	GCGATTCAGGGAGTGTG	GAGCGGCTCTCTTCA	530	
Qy	301	agaaac	ccactcagacac	tgctcagctcgtcctcaaat	gccgaaagaaatgggtcaggt	360	
Db	531	AGAAAC	ACCACTCAGACAC	TGCCCTCAGCTGCTCAAAT	GCCGAAGGAATGGGT	590	
Qy	361	ggagat	ctctcttgccacagt	ggaccggggacacgctgtg	tgctgcagaaagaaaccagta	420	
Db	591	GGAGAT	CTCTCTGTCACAGT	GGACCGGGACACCGTGTG	TGGCTGCAGAGAACCA	650	
Qy	421	ccggcat	tattggagtgaaac	cttttccagtgcttcaattg	cagcctctgcctcaatgg	480	
Db	651	CCGGCA	TATTGGAGTCAAAAC	CTTTTCCAGTGTCTCAAT	TGCAGCCTCTGCCTCA	710	
Qy	481	gacggt	gcacctctcctgtc	caggagaaaaacagacac	gcgtgtgcacctgcctgcaggttt	540	
Db	711	GACCGT	GCACCTCTCTTCC	TGCCAGAGAAACAGAC	ACCGTGTGCACCTGCCAT	770	
Qy	541	cttctaa	gaaaaaacagtgctc	ctctagttaactgaaagaa	gcctgcagtgagtcac	600	
Db	771	CTTTCT	TAGAGAAACAGAGTGT	CTCTCTAGTAACTGTAA	GAAAGCCTGGAGTGCAC	830	
Qy	601	gaagtt	gtgctacc	ccagattgagaatgt	taagggcactgaggactc	caggcaccacagt	660
Db	831	GAAGTT	GTGCTACCC	CAGATTGAGAAATGTT	TAGGGCACTGAGCACT	CGAGCAACACAGT	890
Qy	661	gctgtg	ccctcgtgttcgt	tcctcagccttttcc	cagtgcat	aaagcaggtttttttttgtt	720
Db	891	GCTGTG	CGCCCTGGTCATTT	CTTTGGTCTTTGCC	TTTTATCCCTCTCT	TCATTGGTTT	950
Qy	721	tttgttt	ttgtt	731			
Db	951	AATGAT	TCGTT	961			

RESULT	10
A78738	
LOCUS	DNA
DEFINITION	Sequence 7 from Patent EP0568925.
ACCESSION	A78738
VERSION	A78738.1 GI:6090341
KEYWORDS	.
SOURCE	unidentified.
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 2175)
TITLE	Brakebusch,C. and Wallach,D.
JOURNAL	TNF RECEPTOR ACTION MODULATION
	Patent: EP 0568925-A 7 10-NOV-1993;
FEATURES	YEDA RES & DEV (IL)
	location/Qualifiers
source	1..2175
	/organism="unidentified"
	/db_xref="taxon:32644"
BASE COUNT	474 a 641 c 604 g 456 t
ORIGIN	

Query Match	79.2%	Score	676.6;	DB	9;	Length	2175;	
Best Local Similarity	95.3%	Pred. No.	4.2e-178;					
Matches 697;	Conservative	0;	Mismatches	34;	Indels	0;	Gaps	0;

Qy 1 gagtggaggccatagctgctggcatgggctctccaccgtgctgaactgctgtgcc 60
|||||
Db 231 GAGTGAAGAGCCCA"AGC"TGCTGGCAATGGGCTCTCCACCGTGCC"GC"GTGCTGCC 290

Qy	61	gctgggtcctcgtgagctgttggctgggaatatataccctccaggggttatttgagctggtccc	120
Db	291	GCTGGTGTCTCTGGAGCTGTTGGTGGGAATATATACCCCTCAGGGGTATTATGGACTGGTCCC	350
Qy	121	tcacctaggggacagggaagaagatagttgtgtgtccccaaggaaaaatatatccacc	180
Db	351	TCACCTAGGGGACAGGGAGAAGAGAGATAGTGTGTGTCCCAACAGGAAAAATATATPCACCC	410
Qy	181	tcaataatacttgctgtctacaaagtgcacaaaggaaacctacttgttacaatgactg	240
Db	411	TCAAAATAATTTCGATTGCTGTACCAAGTGCACAAAGGAACCTACTTGTACAAATGACTG	470
Qy	241	tccaggccggggcaggatagacacgtcagggagctgagagcggtcctctccacgcttc	300
Db	471	TCCAGGCCCGGGCAGGATACGGACTCAGGGAGTGTGAGAGCGGCTCCTTTCAACCGCTTC	530
Qy	301	agaaaaacacctcagacaactcctcagctgctccaatatgcgaaaggaaaaatgggtcaggt	360
Db	531	AGAAACACACCTCAGACACTGCCCTCAGCTGCTCCAAATGCCAAAGGAAATGGGTCAAGT	590
Qy	361	ggagatcctctcttcacagtggaccgggacacagtgctggtctgcaggagaacacagta	420
Db	591	GGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACACAGTA	650
Qy	421	ccggcattattggagtgaataacctttccagtgcttcaattgcagcctctgcctcaatgg	480
Db	651	CCGGCATTTATTGGAGTGAAAAACCTTTTCCAGTGTCTCAATTGCAGCCTCTGCCTCAATGG	710
Qy	481	gaccgtgcacctctctcgtccaggagaaacagaaacacogtgtgcacctgccaatgcaggttt	540
Db	711	GACCGTGCACCTCTCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGGTTT	770
Qy	541	ctttctaagagaataacagagtgtgtctcctgtagtaactgtaaagaaaacctggagtgcac	600
Db	771	CTTTCTAAGAGAAAAACGAGTGTGTCTCCTGTAGTAACTGTGAAGAAAAACCGCTGGAGTGCAC	830
Qy	601	gaagtgtgcctaccacagattgagaatgttaagggcactgaagacctcaggaccacagtt	660
Db	831	GAAGTGTGTGCCCTACCCAGATGTGAATGTTTAAGGGCACCTGAGGACCTCAGGCACACACAGT	890
Qy	661	gctgtgccccttggtctogtccctgagcctttttcacagtgcaataagcagttttttttgtt	720
Db	891	GCTGTGGCCCTGGTCACTTTTCTTGGTCTTTGGCTTTTATCCCTCCTCTTCATTGGTTT	950
Qy	721	tttgttttgttt 731	
Db	951	AATGATACGCT 961	

[illegible]

Query Match	79.28;	Score 676.6;	DB 9;	Length 2175;
-------------	--------	--------------	-------	--------------

AUTHORS Wallach,D.; Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D.
TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-1)
JOURNAL Patent: EP 0433900-A 28 JUN-1991;
YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED

FEATURES Location/Qualifiers

source
1. 2176
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 474 a 642 c 604 g 456 t

ORIGIN

Query Match 79.2%; Score 676.6; DB 9; Length 2176;
Best Local Similarity 95.3%; Pred. No. 4.2e-178;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 gagtgagagccatagctgtctggcatgggcccctccaccctgctgacctgctgtctgcc 60
Db 231 GAGTGAGAGGCCATAGCTGTGTCATGGGGCTCTCCACCGTGCCTGACCTGCTGCTGCC 290

Qy 61 gctgtgctcctgagctgtgtgggaataataaccctcagggttattgactgtctcc 120
Db 291 GCTGTGCTCTCTGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 350

Qy 121 tcacctggggacaggagagagatagtggtgtcccaagaaataatatcaccc 180
Db 351 TCACCTAGGGACAGGAGAGAGATAGTGTGTCCCAAGAAATATATCCACCC 410

Qy 181 tcaaaataattcgatttgctgtaccagtgcccaaggaaacctacttgtaaatgactg 240
Db 411 TCAAAATAATTTCGATTTCCTGTACCAAGTGCCACAAAGAACTACTTGTACAATGACTG 470

Qy 241 tccaggccggggcagatcagctgagtgagtgagcggctcctccacgcttc 300
Db 471 TCCAGGCCGGGGCAGATACGGACTGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTC 530

Qy 301 agaaaacacacctcagacactgcctcagctgtccaaatgccgaaggaaatgggtcaggt 360
Db 531 AGAAACACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAGGAATGGGTGAGT 590

Qy 361 ggaagatctcttctgacagtggaacgggacacccgtgtgtgctgcaggaagaccagta 420
Db 591 GGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTA 650

Qy 421 ccggcattattggagtgaaaacctttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 651 CCGGCATATTGGAGTGAAACCTTTTCCAGTGTCTCAATTGACGCCCTGCTGCTCAATGG 710

Qy 481 gaccgtgcacctctcctgcaggagaaacagacacccgtgtgcacctccatgcaggttt 540
Db 711 GACCGTGACCTCTCTCTGCCAGGAGAAACACACCCGTGTGCACCTGCCATGCGAGGTT 770

Qy 541 ctttctaagagaacacagtgctgtctcctgtagtaactgtgaagaaagcctggagtgac 600
Db 771 CTTTCTAAGACAAACAGTGTCTCTCTGTAGTAACGTGAAGAAAGCCCTGGAGTGCAC 830

Qy 601 gaagtgtgctactcccagatgtgaagtgttaaggggcactgaggactcaggcaccacagt 660
Db 831 GAAGTTGTGCTTACCCAGATGTGAATGTGTAAGGGCCTACTGAGGACTCAGGCACACAGT 890

Qy 661 gctgttcccctggttccctgagcctttttcacagtgcataagcagtttttttttt 720
Db 891 GCTGTGCCCTGTGTCATTTTCTTTGGTCTTTTGCTTTTATCCCTCTCTCTATTGGTTT 950

Qy 721 ttgtttttgtt 731
Db 951 AATGATATCGCT 961

RESULT 14
A29103

LOCUS A29103 1331 bp DNA PAT 03-JUL-1995
DEFINITION H.sapiens mRNA for TNF-binding polypeptide from patent EP0393438.
ACCESSION A29103
VERSION A29103.1 GI:1247517
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1331)
AUTHORS Hauptmann,R., Himmeler,A., Maurer-Pogy,I. and Stratowa,C.
TITLE TNF-receptor, TNF-binding protein and DNA coding therefor
JOURNAL Patent: EP 0393438-A 53 24-OCT-1990;
BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H.

FEATURES Location/Qualifiers

source
1. 1331
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 298 a 407 c 343 g 283 t

ORIGIN

Query Match 79.0%; Score 675; DB 9; Length 1331;
Best Local Similarity 95.2%; Pred. No. 1.1e-177;
Matches 696; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 1 gagtgagagccatagctgtctggcaatggcctccaccgtcctgacctgctgtctgcc 60
Db 188 GAGTGAGAGGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCC 247

Qy 61 gctgtgctcctggagctgttgggggaataataaccctcagggttattgactgtctcc 120
Db 248 ACTGTGCTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 307

Qy 121 tcaactaggggacaggagaaagagatagtggtgtcccaagaaataatatcaccc 180
Db 308 TCACCTAGGGGACAGGAGAGAGATAGTGTGTCCCCAAGGAAATATATCCACCC 367

Qy 181 tcaaaataattcgatttgctgtaccagtgcccaaggaaacctacttgtaaatgactg 240
Db 368 TCAAAATAATTTCGATTTCCTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTG 427

Qy 241 tccaggccggggcaggaatcagctgtgagtgagcggctcctccacgcttc 300
Db 428 TCAGGCCCGGGCAGGATACGGACTGCAGGGAGTGTGAGAGCGGCTCTCTACCGCTTC 487

Qy 301 agaaaacacacctcagacactgcctcagctgtccaaatgccgaaggaaatgggtcaggt 360
Db 488 AGAAACACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAGGAATGGGTGAGT 547

Qy 361 ggaagatctcttctgacagtggaacgggacacccgtgtgtgctgcaggaagaccagta 420
Db 548 GGAGATCTCTTCTTGCACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTA 607

Qy 421 ccggcattattggagtgaaaaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 608 CCGGCATATTGGAGTGAAACCTTTTCCAGTGTCTCAATTGACGCCCTGCTGCTCAATGG 667

Qy 481 gaccgtgcacctctcctgcaggagaaacagacacccgtgtgcacctgcacatgcaggttt 540
Db 668 GACCGTGCACCTCTCTCTGCCAGGAGAAACAGACACCGTGTGCACCTGCGCATGCAGGTTT 727

Qy 541 ctttctaagagaacacagtgctgtcctgtagtaactgtgaagaaagcctggagtgac 600
Db 728 CTTTCTAAGAGAAACAGTGTGTCTCTGTAGTAACGTGAAGAAAGCCCTGAGTGCAC 787

Qy 601 gaagtgtgctactcccagatgtgaagtgttaaggggcactgaggactcaggcaccacagt 660
Db 788 GAAGTTGTGCTTACCCAGATGTGAATGTGTAAGGGCCTACTGAGGACTCAGGCACACAGT 847

Qy 661 gctgttcccctggttccctgagcctttttcacagtgcataagcagtttttttttt 720
Db 848 GCTGTGCCCTGTGTCATTTTCTTTGGTCTTTTGCTTTTATCCCTCTCTCTATTGGTTT 907


```
QY 721 ttgtttttgtt 731
| | | | |
Db 908 AATGTATCGCT 918

RESULT 15
HUMTNFRC
LOCUS 2112 bp mRNA PRI 03-AUG-1993
DEFINITION Human tumor necrosis factor receptor (TNF receptor) mRNA, complete
cgs.
ACCESSION M63121 M75861
VERSION M63121.1 GI:339755
KEYWORDS tumor necrosis factor receptor.
SOURCE Human cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2112)
AUTHORS Himmler,A., Maurer-Fogy,I., Kroenke,M., Scheurich,P.,
pfizenmaier,K., Lantze,M., Olsson,I., Hauptmann,R., Stratowa,C. and
Adolf G.R.
TITLE Molecular cloning and expression of human and rat tumor necrosis
factor receptor chain (p60) and its soluble derivative, tumor
necrosis factor-binding protein
JOURNAL DNA Cell Biol. 9, 705-715 (1990)
MEDLINE 91090841
FEATURES
source
location/Qualifiers
1..2112
/organism="Homo sapiens"
/db_xref="taxon:9606"
207..293
/feature="TNF receptor"
207..1574
/feature="TNF receptor"
/codon_start=1
/product="tumor necrosis factor receptor"
/protein_id="AAA36754.1"
/db_xref="GI:339756"
/translation="MGLSTVPDLLLVLELLVGIYPSGVIGLVPHLGDRKRSVC
POGKYIHQNNISICTCKHKGYLYNDQPGPGQDDCEGSGFASSENHLRLCLSC
SKCRKEMQVRISSCTVDRTVCGCKRQRYHWSNLFQCFNCSCLNGTVHLSCQE
KONTVCTAGCFILRENECVCSNCKSLECKLCLPOLENKVGTFEDSGTTLPLVI
FFGLCLSLGILMYRQWKSKLYSIVCGKSTPEKEGELGTTTKPLAPNPSPT
PGFTPLGFSVPSTFTSSSTYTPGDCPNAPREVAAPPYQGDPIALALASDPI
FNPLQWEDSAHKPOSLOTDTPATLYAVVENPPLRWKEFVRRLGLSDEIDRLLEQN
GRCLREAOYSMLATWRRRTPREATLELLGRVLRDMLGLCLEIDIEALCGPAALPPA
PSLLR"
207..1574
/feature="TNF receptor"
294..1571
/feature="TNF receptor"
/product="tumor necrosis factor receptor"

BASE COUNT 435 a 632 c 589 g 456 t
ORIGIN
```

```
Query Match 79.0%; Score 675; DB 97; Length 2112;
Best Local Similarity 95.2%; Pred. No. 1.2e-177;
Matches 696; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 gaggtagagccatagctgtctggcatggcgctctccacgcctgcctgacctgtgtgccc 60
| | | | |
Db 182 GAGTGAGAGCCATAGCTGTCTGGCATGGGCTCTCCACCGTGCCTGCCTGCTGCTGCC 241
| | | | |

QY 61 gctgtgtctcctggagctgttgggaataataaccctcaggggttatggacctgtccc 120
| | | | |
Db 242 ACTGGTGCCTCCCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 301
| | | | |

QY 121 tcacctagggagcagagagagatagctgtgtgtcccaaggagaaatatatccacccc 180
| | | | |
Db 302 TCACCTAGGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATAATATATCCACC 361
| | | | |
```

Search completed: August 14, 2001, 06:18:24
Job time: 2476 sec

1	676.6	79.2	2062	13	AAQ20973	TNF- α binding
2	676.6	79.2	2062	13	AAQ24440	Encodes TNF- α
3	676.6	79.2	2088	12	AAQ10883	30kD TNF inhibitor
4	676.6	79.2	2088	22	AAC83946	Human 30 kDa TNF i
5	676.6	79.2	2111	12	AAQ10955	Encodes human 55kD
6	676.6	79.2	2111	20	AAZ09170	Human tumour necro
7	676.6	79.2	2161	21	AAZ48475	Human tumour necro
8	676.6	79.2	2175	16	AAQ90513	Human tumour necro
9	675	79.0	1334	11	AAQ06282	p55 TNF-R gene. H
10	675	79.0	2176	12	AAQ12215	Plasmid Tumour Nec
11	673.4	78.9	2170	14	AAQ50870	Type I TNF recepto
						p55 Tumour necrosi

CC sequenced. The coding region of the majority of the human TNF-alpha
CC 55kd receptor was isolated as an EcoRI fragment encoding 374 amino
CC acids, and cloned into a mammalian cell expression vector, resulting
CC in pTNFR. A derivative of the TNF-alpha receptor was produced by
CC engineering a termination codon just prior to the transmembrane
CC domain. PCR with primers AAQ29237.8 generated a 300bp
CC restriction fragment which was cloned into pTNFR, giving pTNFRcd.
CC DNA sequencing confirmed this contained the designed DNA sequence.
CC The TNF-alpha receptor expression plasmids were then transfected
CC into monkey COS-7 cells.
CC See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8
XX
XX Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T; 0 other;

Query Match 79.2%; Score 676.6; DB 13; Length 2062;
Best Local Similarity 95.3%; Pred. No. 1.8e-162;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 gagtgagagccatagctgtctggcatggcgctctccacgctgcctgacctgtctgtgcc 60
DB 130 gagtggagccatagctgtctggcatggcgctctccacgctgcctgacctgtctgtgcc 189
QY 61 gctgtgctctgagctgtgttggtgggaataatccctcaggggtattgagctgtctcc 120
DB 190 gctgtgctctgagctgtgttggtgggaataatccctcaggggtattgagctgtctcc 249
QY 121 tcacctaggagcagaggaagagagatagtggtgtcccaaggaataatccaccc 180
DB 250 tcacctaggagcagaggaagagagatagtggtgtcccaaggaataatccaccc 309
QY 181 tcaaaataatctgattgtctgaccagtgcccaaggaacactactgtacaaatgactg 240
DB 310 tcaaaataatctgattgtctgaccagtgcccaaggaacactactgtacaaatgactg 369
QY 241 tccagcccgccgagcagctgacgagtgagtgagcggcgctctccacgcttc 300
DB 370 tccagcccgccgagcagctgacgagtgagtgagcggcgctctccacgcttc 429
QY 301 agaaacacccctcagacactgctctgctgtcccaatgcccgaaggaataatggctcaggt 360
DB 430 agaaacacccctcagacactgctctgctgtcccaatgcccgaaggaataatggctcaggt 489
QY 361 ggagatctctctgacagtgacgggagacacgctgtgtggtgcaggaagacagta 420
DB 490 ggagatctctctgacagtgacgggagacacgctgtgtggtgcaggaagacagta 549
QY 421 ccggcattattggagtgaaaaacctttccagtgcttcaattgcagcctctgcctcaatgg 480
DB 550 ccggcattattggagtgaaaaacctttccagtgcttcaattgcagcctctgcctcaatgg 609
QY 481 gaccgtgacctctctgccagagagaacacacacgctgtgcacctgacctgcaggttt 540
DB 610 gaccgtgacctctctgccagagagaacacacacgctgtgcacctgacctgcaggttt 669
QY 541 ctttctaagagaacagagtggtgtctctctgtagtaactgtaagaaaagcctggagtcac 600
DB 670 ctttctaagagaacagagtggtgtctctctgtagtaactgtaagaaaagcctggagtcac 729
QY 601 gaagttgtgctaccacagattgagaatgttaaggcagctgaggaactcaggaccacagtt 660
DB 730 gaagttgtgctaccacagattgagaatgttaaggcagctgaggaactcaggaccacagtt 789
QY 661 gctgttgccctggttgcgtccctgagccttttccagtgcatagacagttttttttgtt 720
DB 790 gctgttgccctggttgcattttttttgttggcttttgccttttccctctctcttctt 849
QY 721 ttgtttttgtt 731
DB 850 aatgtatcgct 860

RESULT 3

AAQ10883
ID AAQ10883 standard; cDNA; 2088 BP.
XX
XX AAQ10883;
XX AC
XX 13-MAY-1991 (first entry)
XX 30kd TNF inhibitor precursor gene in lambda-gtl0-7ctnfbp.
XX Tumour necrosis factor; inhibitor; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 171..1536
XX /*tag= a
XX
XX AU9058976-A.
XX 24-JAN-1991.
XX 16-JUL-1990; 90AU-0058976.
XX 07-FEB-1990; 90US-0479661.
XX 18-JUL-1989; 89US-0381080.
XX 11-DEC-1989; 89US-0450329.
XX (SYNE-) SYNERGEN INC.
XX WFI; 1991-073847/11.
XX P-PSDB; AAR10986.
XX
XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha
XX and -beta, useful as therapeutic agent.
XX
XX Disclosure; Fig 21; 142pp; English.
XX
XX The sequence encodes the entire 30 kd TNF inhibitor. The clone from
XX which the sequence was obtd. was isolated from a cDNA library
XX prepd. from RNA form U937 cells treated with PMA/PHA. The whole
XX gene can be inserted into expression vectors for prepn. of TNF
XX inhibitor for use in the treatment of inflammatory and degenerative
XX diseases.
XX See also AAQ10878, AAQ10884 and AAQ10907.
XX
XX Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;

Query Match 79.2%; Score 676.6; DB 12; Length 2088;
Best Local Similarity 95.3%; Pred. No. 1.8e-162;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 gagtggagccatagctgtctggcatggcgctctccacgctgcctgacctgtctgtgcc 60
DB 144 gagtggagccatagctgtctggcatggcgctctccacgctgcctgacctgtctgtgcc 203
QY 61 gctgtgctctgagctgtgttggtgggaataatccctcaggggtattgagctgtctcc 120
DB 204 gctgtgctctgagctgtgttggtgggaataatccctcaggggtattgagctgtctcc 263
QY 121 tcacctaggagcagaggaagagagatagtggtgtcccaaggaataatccaccc 180
DB 264 tcacctaggagcagaggaagagagatagtggtgtcccaaggaataatccaccc 323
QY 181 tcaaaataatctgattgtctgtaccagtgcccaaggaacactactgtacaaatgactg 240
DB 324 tcaaaataatctgattgtctgtaccagtgcccaaggaacactactgtacaaatgactg 383
QY 241 tccagggcccgccgagcagctgacgagtgagtgagcggcgtctcctcaccgcttc 300
DB 384 tccagggcccgccgagcagctgacgagtgagtgagcggcgtctcctcaccgcttc 443
QY 301 agaaacacccctcagacactgcctcagctgtctccaaatgccgaaggaataatgggtcaggt 360

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
XX WPI: 1999-480840/41.
DR P-PSDB; AAY30934.
XX
XX New insoluble proteins, and fragments, that bind to tumor necrosis
PT factor, used to treat e.g. septic shock or cerebral malaria
XX
XX Claim 4; Fig 1; 25pp; German.
XX
XX This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (Ia) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (i) and (ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (ant)agonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (I) are used for affinity purification of (I). This sequence encodes
CC a tumour necrosis factor binding protein described in the method of
CC the invention.
XX
XX Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;

Query Match 79.2%; Score 676.6; DB 20; Length 2111;
Best Local Similarity 95.3%; Pred. No. 1.8e-162;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 gaggtagagggccatagctgtctgcatgggctctccacgtgctgacctgctgctgcc 60
DB 162 gaggtagagggccatagctgtctgcatgggctctccacgtgctgacctgctgctgcc 221
QY 61 gctggtgctctgagctgtgtgggaatacaccctcagggtgtattggactgtgcc 120
DB 222 gctggtgctctgagctgtgtgggaatacaccctcagggtgtattggactgtgcc 281
QY 121 tcacctaggggacaggggagagagatagtggtgtgtcccaaggaaatatatccacc 180
DB 282 tcacctaggggacaggggagagagatagtggtgtgtcccaaggaaatatatccacc 341
QY 181 tcaaaataatcgtattgtctgtaccagtgccaaagtgccaaagaaacctactgtacaaatgactg 240
DB 342 tcaaaataatcgtattgtctgtaccagtgccaaagtgccaaagaaacctactgtacaaatgactg 401
QY 241 tccaggcccgggcaggatagcaggtcagggagtggtgagagcggtctctccacgcttc 300
DB 402 tccaggcccgggcaggatagcaggtcagggagtggtgagagcggtctctccacgcttc 461
QY 301 agaaacacacctcctcagactgctcagctgtctccaaatgccgaaggaaatgggtcaggt 360
DB 462 agaaacacacctcctcagactgctcagctgtctccaaatgccgaaggaaatgggtcaggt 521
QY 361 ggagatctctctgtcacagtggacggggagacacgtgtgtggtgctcaggaaagacagta 420
DB 522 ggagatctctctgtcacagtggacggggagacacgtgtgtggtgctcaggaaagacagta 581
QY 421 ccggcattattggagtgaaacacctttccagtgtctcaattgacacgtctgctccaatgg 480
DB 582 ccggcattattggagtgaaacacctttccagtgtctcaattgacacgtctgctccaatgg 641
QY 481 gacgtgacacctctcctcggaggagaaacagaaacacgtgtgtcactgcatgacaggttt 540
DB 642 gacgtgacacctctcctcggaggagaaacagaaacacgtgtgtcactgcatgacaggttt 701
QY 541 ctttctaagaaacagagtggtgtctctctgtagtaactgtgaagaaagcctggagtgac 600
DB 702 ctttctaagaaacagagtggtgtctctctgtagtaactgtgaagaaagcctggagtgac 761

QY 601 gaagttgtcctaccaccagattgagaatgttaagggcactgagactcagccaccacagt 660
DB 762 gaagttgtcctaccaccagattgagaatgttaagggcactgagactcagccaccacagt 821
QY 661 gctgttgcccttgctgctccctgagccctttttcacagtgataaagcaggtttttttgtt 720
DB 822 gctgttgcccttgctgctccctgagccctttttttgtgtgtcttctcctctctcattgtgtt 881
QY 721 ttgtgtttgtt 731
DB 882 aatgtatcgtc 892

RESULT 7
AAZ48475
ID AAZ48475 standard; DNA; 2161 BP.
XX
AC AAZ48475;
XX
DT 31-MAR-2000 (first entry)
XX
DE Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
XX inflammation; tumour formation; TNFR1; anticancer; ds.
XX
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PF 26-JUN-1998; 98US-0106038.
XX
PR 26-JUN-1998; 98US-0106038.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Baker BP, Cowser LM;
XX
XX WPI: 2000-105333/09.
XX
XX Antisense inhibition of tumor necrosis factor type 1 expression for
PT diagnosis, treatment and prevention of disease, particularly tumors
XX
XX Example 10; Columns 33-36; 34pp; English.
XX
XX The invention provides antisense compounds targeted to human tumour
CC necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC can be used in a method of inhibiting the expression of TNFR1 human cells
CC or tissues. The antisense compounds specifically hybridize with one or
CC more nucleic acids encoding TNFR1 modulating the function of nucleic
CC acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC produced. The antisense compounds and method are useful as research
CC reagents and diagnostics, and in the treatment and prophylaxis of
CC infection, inflammation or tumour formation. The present sequence
CC represents the nucleotide sequence of human TNFR1 (Genbank Accn No:
CC X55313).
XX
XX Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;

Query Match 79.2%; Score 676.6; DB 21; Length 2161;
Best Local Similarity 95.3%; Pred. No. 1.8e-162;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 gaggtagagggccatagctgtctgcatgggctctccacgtgctgacctgctgctgcc 60
DB 231 gaggtagagggccatagctgtctgcatgggctctccacgtgctgacctgctgctgcc 290
QY 61 gctggtgctcctgagctgtgtgggaatacaccctcaggggttattggactgtgcc 120
DB 291 gctggtgctcctgagctgtgtgggaatacaccctcaggggttattggactgtgcc 350


```

XX AC AAQ12215;
XX 12-SEP-1991 (first entry)
XX Type I TNF receptor.
XX Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT terminator 244..246
FT /*tag= a
FT /*note= "in-frame termination codon"
FT CDS 256..1620
FT /*tag= a
FT /*product= type I TNF receptor
FT sig_peptide 256..318
FT /*tag= b
FT mat_peptide 319..1620
FT /*tag= c
FT misc_RNA 319..864
FT /*tag= d
FT /*label= soluble_domain
FT /*note= "may be 2 codons shorter or a few codons longer"
FT misc_feature 376..414
FT /*tag= e
FT /*note= "TBP-I derived sequence"
FT misc_feature 583..627
FT /*tag= f
FT /*note= "TBP-I derived sequence"
FT misc_feature 850..858
FT /*tag= g
FT /*note= "TBP-I derived sequence"
FT misc_RNA 889..957
FT /*tag= h
FT /*label= transmembrane_domain
FT repeat_unit 385..504
FT /*tag= i
FT /*number= 1
FT repeat_unit 505..633
FT /*tag= j
FT /*number= 2
FT repeat_unit 634..756
FT /*tag= k
FT /*number= 3
FT repeat_unit 757..858
FT /*tag= l
FT /*number= 4
FT polyA_signal 2145..2150
FT /*tag= m
XX PN EP433900-A.
XX 26-JUN-1991.
XX PF 13-DEC-1990; 90EP-0124133.
XX 12-JUL-1990; 90IL-0095064.
XX PR 13-DEC-1989; 89IL-0092697.
XX (YEDA ) YEDA RES & DEV CO LTD.
XX Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
XX Aderka D;
XX WPI; 1991-186774/26.
XX P-PSDB; AAR12550.
XX Recombinant tumour necrosis factor binding protein I - prepd. by
XX transfecting eukaryotic cells with vector contg. deoxyribonucleic

```

```

PT acid encoding human type T TNF receptor or soluble domain
XX Disclosure; Fig 1(D); 30pp; English.
XX The Tumour Necrosis Factor Binding Protein I is the soluble form of
XX type I TNF-receptor and constitutes a fragment of the cell surface
XX form of this receptor, corresp. to its extracellular domain.
XX There is no characteristic poly(A) addition signal near the 3' end
XX of the cDNA. The sequence ACTAAA (tag m) may serve as an
XX CC alternative to this signal, but with low efficiency.
XX See also AAQ12212-15.
XX SQ Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T; 0 other;

Query Match 79.0%; Score 675; DB 12; Length 2176;
Best Local Similarity 95.2%; Pred. No. 4.6e-162;
Matches 696; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 gagtgaagagccatagctgtcgtgcatggcgctctccacgctgctgacctgctgctgcc 60
   |||||||
Db 231 gagtgaagagccatagctgtcgtgcatggcgctctccacgctgctgacctgctgctgcc 290

QY 61 gctggtgctcctgagctgtgtgtggaatataccctcaggggttatgtgactggctccc 120
   |||||||
Db 291 gctggtgctcctgagctgtgtgtggaatataccctcaggggttatgtgactggctccc 350

QY 121 tcacctagggagcagggagagagagatagtgtgtcccaagaaaataataccacc 180
   |||||||
Db 351 tcacctagggagcagggagagagatagtgtgtcccaagaaaataataccacc 410

QY 181 tcaaaataatcgtattgtgtaccagtgccacaaaggaaacactactgtacaatgactg 240
   |||||||
Db 411 tcaaaataatcgtattgtgtaccagtgccacaaaggaaacactactgtacaatgactg 470

QY 241 tccaggcccggggcagagatagcaggactgcaggagtggtgagagcgctctcaccgcttc 300
   |||||||
Db 471 tccaggcccggggcagagatagcaggactgcaggagtggtgagagcgctctcaccgcttc 530

QY 301 agaaaaccacctcagacacactgcctcagctcctcaaatgcgaagaaatgggtcaggt 360
   |||||||
Db 531 agaaaaccacctcagacacactgcctcagctcctcaaatgcgaagaaatgggtcaggt 590

QY 361 ggagatctctctgacagtggaacgggacacacgctgtgtgctgcaggaagaaacagta 420
   |||||||
Db 591 ggagatctctctgacagtggaacgggacacacgctgtgtgctgcaggaagaaacagta 650

QY 421 ccggcattattggagtgaataacccctttccagtgcttcaattgcagcgctctgcctcaatgg 480
   |||||||
Db 651 ccggcattattggagtgaataacccctttccagtgcttcaattgcagcgctctgcctcaatgg 710

QY 481 gaccgtgacacctctcctgccaggagaaacagaaacacacgctgtgcacctgcctgaggttt 540
   |||||||
Db 711 gaccgtgacacctctcctgccaggagaaacagaaacacacgctgtgcacctgcctgaggttt 770

QY 541 ctcttaagagaaaaacgagtgctcctcctgtagtaactgtaagaaaaagcctggagtgac 600
   |||||||
Db 771 ctcttaagagaaaaacgagtgctcctcctgtagtaactgtaagaaaaagcctggagtgac 830

QY 601 gaagtgtgctaccgccagattgagaatgttaaggcgactgagactcagcagcacacagt 660
   |||||||
Db 831 gaagtgtgctaccgccagattgagaatgttaaggcgactgagactcagcagcacacagt 890

QY 661 gctgttgccctggttgcctgcctgagcctttttcacagtgatagaagcagttttttgttt 720
   |||||||
Db 891 gctgttgccctggttgcctgagcctttttttgttgccttttatccctcctcttcattggttt 950

QY 721 ttgtttttgtt 731
   |||||
Db 951 aatgtatcgt 961

RESULT 11

```

ID	AAQ050870 standard; DNA; 2170 BP.
XX	AAQ050870;
XX	AC
XX	AC
DT	13-MAY-1994 (first entry)
XX	p55 Tumour necrosis factor receptor coding sequence.
DE	TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW	rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
KW	effector protein; ss.
XX	Homo sapiens.
OS	
XX	Key Location/Qualifiers
FH	256..1623
FT	/tag= a
FT	/product= p55 Tumour necrosis factor receptor.
EP	568925-A.
XX	10-NOV-1993.
XX	29-APR-1993; 93EP-0106981.
XX	03-MAY-1992; 92IL-0101769.
XX	(YEDA) YEDA RES & DEV CO LTD.
PA	Brakebusch C, Wallach D;
PI	WPI; 1993-353057/45.
DR	P-PSDB; AAR42197.
XX	Modulating activity of tumour necrosis factor receptor - using peptides(s), antibodies, etc. which interact with critical regions of receptor or effector protein, for controlling auto-immune disease, septic shock, etc.
XX	Claim 2; Figure 1; 17pp; English.
PS	Modification of the tumour necrosis factor receptor by mutation or deletion modulates signal transduction and/or cleavage effected by the receptor. This modulation of activity can also be achieved using effector proteins which interact with the TNF receptor. CC Molecules which interact with the TNF receptor or the effector CC proteins can be used to treat or prevent diseases associated with CC TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft CC rejection; graft vs. host disease or septic shock. They can also CC be used to treat overdoses of exogenous TNF.
XX	Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T; 0 other;
SQ	
Query Match	78.9%; Score 673.4; DB 14.; Length 2170;
Best Local Similarity	95.1%; Pred. No. 1.2e-161;
Matches 695; Conservative	0; Mismatches 36; Indels 0; Gaps 0;
QY	1 gagtggagagccatgctgttgcctggccttcacaccgtgacctgctgctgcc 60
Db	231 gagtggagagccatgctgttgcctggccttcacaccgtgacctgctgctgcc 290
QY	61 gctgggtgctcctggagctgttggtgggaataatacccctcagggttatggactggctcc 120
Db	291 gctgggtgctcctggagctgttggtgggaataatacccctcagggttatggactggctcc 350
QY	121 tcacctaggagcacgagagaagagatggtgtgtccccaagaaatatatccacc 180
Db	351 tcacctaggagcacgagagaagagatggtgtgtccccaagaaatatatccacc 410
QY	181 tcaaaaaaatctgatttgcgttaccaagtgcacaaggaacctacttgtacaatgactg 240

XX	RESULT 13
XX	AAQ49932
ID	AAQ49932 standard; cDNA to mRNA; 1368 BP.
XX	XX
XX	AAQ49932;
XX	AC
XX	DT
XX	29-APR-1994 (first entry)
XX	DE
XX	Lambda-derived TNF-R cDNA.
XX	XX
KW	Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW	IL-1R; fusion protein; linker: TNF; IL-1; cachexia; cerebral malaria;
KW	rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW	pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW	graft verses host disease; sepsis; inflammation; allergy;
KW	autoimmune dysfunction; ss.
XX	XX
OS	Homo sapiens.
OS	Lambda-gt10-7-ctfbbp.
XX	XX
XX	Key Location/Qualifiers
FF	CDS 1..1366
FT	FT /*tag= a
FT	FT /product= hTNF-R
FT	FT 1..120
FT	FT /*tag= b
FT	FT 121..1363
FT	FT /*tag= c
XX	XX
XX	WO9319777-A.
PN	XX
PD	14-OCT-1993.
XX	XX
XX	26-MAR-1993; 93WO-US02938.
XX	XX
PR	30-MAR-1992; 92US-0860710.
XX	XX
PA	(IMMV) IMMUNEX CORP.
XX	XX
XX	Smith CA;
XX	XX
DR	WPI; 1993-336592/42.
XX	P-PSDB; AAR42059.
XX	XX
PT	New fusion protein tumour necrosis factor and human interleukin-1
PT	receptor - useful in therapy, diagnosis and assays of e.g.
PT	rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX	XX
PS	Disclosure; Page 57-59; 85pp; English.
XX	XX
CC	The sequences given in AAQ49931-32 encode human tumour necrosis factor
CC	receptor (TNF-R) and the sequences in AAQ49933-34 encode human
CC	interleukin-1 receptor (IL-1R). These sequences were used in the
CC	production of a fusion protein which conformed to one of the
CC	formulae:
CC	TNF-R-linker-TNF-R-linker-IL-1R
CC	IL-1R-linker-TNF-R-linker-TNF-R or
CC	TNF-R-linker-TNF-R
CC	The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC	Ser, Thr and Ala. These linkers separate the individual moieties
CC	by such a distance that each component of the fusion protein is
CC	capable of folding into the secondary or tertiary structure required
CC	for its biological activity. These fusion proteins may be used in
CC	therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC	particularly in conditions in which both TNF and IL-1 play a causative
CC	role. They may be used to treat cachexia, rheumatoid arthritis,
CC	diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC	cerebral malaria, allograft and xenograft rejection in graft verses
CC	host disease, sepsis, septic shock, inflammation, allergies and
CC	autoimmune dysfunctions.
XX	XX
SQ	Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;

CC cause a change in the TNFR1 protein. The TNFR1 polymorphisms may be
CC useful for studying the biological function of TNFR1 as well as for
CC identifying drugs targeting the protein for treatment of disorders
CC related to its abnormal expression or function such as tumours,
CC apoptosis related disorders and bacterial infection.
XX
SQ Sequence 1368 BP: 292 A; 424 C; 376 G; 276 T; 0 other;

Query Match	76.3%;	Score 651.6;	DB 21;	Length 1368;
Best Local Similarity	95.2%;	Pred. No. 3.4e-156;		
Matches 672;	Conservative	0;	Mismatches 34;	Indels 0;
Matches 672;	Conservative	0;	Mismatches 34;	Indels 0;
Matches 672;	Conservative	0;	Mismatches 34;	Indels 0;

QY	26	atgggctctccaccgtgctgacctgctgctgcgcgtgcgcgtggtgctcctgagctgttggtg	85
Db	1	atgggctctccaccgtgctgacctgctgctgcgcgtgcgcgtggtgctcctgagctgttggtg	60
QY	86	ggaatataccctcagggttattgactgggtccctccactcctcagggaacaggagaagaga	145
Db	61	ggaatataccctcagggtgtatgactgggtccctccactcctcagggaacaggagaagaga	120
QY	146	gatagtgtgtccccaagaaataataccaccctcaaaaataattcgatttgcgtgacc	205
Db	121	gatagtgtgtccccaagaaataataccaccctcaaaaataattcgatttgcgtgacc	180
QY	206	aagtgcacaaaagaaacctacttgtacaatgactgtccaggccggcgaggagatacggac	265
Db	181	aagtgcacaaaagaaacctacttgtacaatgactgtccaggccggcgaggagatacggac	240
QY	266	tcaggaggagtgtagagcggctcttcacgcgttcagaaacacacctcagacactgcctc	325
Db	241	tcaggaggagtgtagagcggctcttcacgcgttcagaaacacacctcagacactgcctc	300
QY	326	agctgctccaaatgcgcgaagaaaatggctcagggtgagatctctcttgcacagtggac	385
Db	301	agctgctccaaatgcgcgaagaaaatggctcagggtgagatctctcttgcacagtggac	360
QY	386	cgggacacgctgtgtggctgcaggaagaacacagtacccgattattggagtgaaaacctt	445
Db	361	cgggacacgctgtgtggctgcaggaagaacacagtacccgattattggagtgaaaacctt	420
QY	446	ttccagtgttcaattgcagctcctgcctcctaattggagaccgtgcacctctcctgcaggag	505
Db	421	ttccagtgttcaattgcagctcctgcctcctaattggagaccgtgcacctctcctgcaggag	480
QY	506	aaacagaaacacgctgtgcacctgccatgcaggtttcttctaagagaacacagtgctc	565
Db	481	aaacagaaacacgctgtgcacctgccatgcaggtttcttctaagagaacacagtgctc	540
QY	566	tcctgtagtaactgtaagaaaacgctggagtgcaagagttgtgcctacccacagattggag	625
Db	541	tcctgtagtaactgtaagaaaacgctggagtgcaagagttgtgcctacccacagattggag	600
QY	626	aatgtttaaggggcactgaggactcaggcacacacagtgctgttgcctcgttgcgtccctga	685
Db	601	aatgtttaaggggcactgaggactcaggcacacacagtgctgttgcctcgttgcgtccctc	660
QY	686	gcctttttacagtgcatagaagcagttttttttgtttttgtttttgttt	731
Db	661	qgtcttttgcctttttatccccctccttcattggttttaattatcctgt	706

RESULT 15
AAT15931
ID AAT15931 standard; DNA: 6889 BP.

AA
AC AAT15931;
XX
DT 20-JUN-1996 (first entry)

DE DHFR/intron (WTrasSD)-TnFr-IgG dicistronic vector.

KW Recombinant host cell; dihydrofolate reductase; selectable marker;

KW	DIFR; ras splice donor; dicistronic vector; gene expression;
KW	Immunoadhesin; Tnfr-IgG; tumour necrosis factor; ds.
XX	
XX	Synthetic.
OS	
XX	WO9604391-A1.
PN	
XX	
XX	15-FEB-1996.
PD	
XX	
XX	28-JUL-1995; 95WO-US09576.
PF	
XX	
XX	05-AUG-1994; 94US-0286740.
PR	
XX	
XX	(GETH) GENENTECH INC.
PA	
XX	
XX	Crowley CW;
PI	
XX	
XX	WPI; 1996-129407/13.
DR	
XX	
XX	Improved process for the selection of recombinant host cells
PT	expressing high level of a desired product - uses eukaryotic host
PT	cells contg. a DNA construct comprising a selectable gene
XX	
XX	Example 2; Page 36-42; 137pp; English.
PS	

A dicistronic vector (AAT15930) comprises a regulatory region derived from the cytomegalovirus immediate-early gene, a selectable dihydrofolate reductase gene positioned within an intron having a 5' wild-type ras splice donor site, a downstream sequence coding for an immunoadhesin, Tnfr-IgG, capable of binding tumour necrosis factor, and a poly-A sequence. Transfection of CHO DHFR⁻ cells and subsequent methotrexate amplification and growth of the cells in nutrient-rich medium gave Tnfr-IgG in yields of 9.5 ug/ml (15-fold higher compared to conventional vector amplified pools).

Sequence 6889 BP: 1729 A; 1826 C; 1681 G; 1653 T; 0 other;

Query Match	76.2%	Score 651	DB 17	Length 6889
Best Local Similarity	100.0%	Pred. No. 9.1e-156		
Matches 651	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	9	ggccatagctgtctgtgcattggtgcctctccacgctgcctgacctgctgtgctgcgctggtgc	68
Db	1588	ggccatagctgtctgtgcattggtgcctctccacgctgcctgacctgctgtgctgcgctggtgc	1647
Qy	69	tcttgagctgttgggtgggaataaccctcagggttatttgacctggtccctcacctag	128
Db	1648	tcttgagctgttgggtgggaataaccctcagggttatttgacctggtccctcacctag	1707
Qy	129	gggacagggaagagagatagtgtgtgtccccaaggaaaaatatccaccctcaaaata	188
Db	1708	gggacagggaagagagatagtgtgtgtccccaaggaaaaatatccaccctcaaaata	1767
Qy	189	attcgatttctctaccaagtgccaaaggaaactacttgcacaatgactgtccagccc	248
Db	1768	attcgatttctctaccaagtgccaaaggaaactacttgcacaatgactgtccagccc	1827
Qy	249	cggggcaggatacggactcaggaggtgtgagcggtctctccaccgttcagaaaaacc	308
Db	1828	cggggcaggatacggactcaggaggtgtgagcggtctctccaccgttcagaaaaacc	1897
Qy	309	acctcagaacactgcctcagctgtccaaatgcgaaaaaggaaatgggtcaggtggagatct	368
Db	1888	acctcagaacactgcctcagctgtccaaatgcgaaaaaggaaatgggtcaggtggagatct	1947
Qy	369	ctctctgcagtgagccgggacaccggtgtggtctgaggaagaaccagtcaccggcatt	428
Db	1948	ctctctgcagtgagccgggacaccggtgtggtctgaggaagaaccagtcaccggcatt	2007
Qy	429	attggagtgaacccttttccagtgcttcaattgcagocctctgcctcaatgggaccgtgc	488
Db	2008	attggagtgaacccttttccagtgcttcaattgcagocctctgcctcaatgggaccgtgc	2067

QY 489 acctctcctgccaggagagaacacagaaacaccgtgtgcacctgccatgccaggtttcttcttaa 548
|||||
Db 2068 acctctcctgccaggagagaacacagaaacaccgtgtgcacctgccatgccaggtttcttcttaa 2127
|||||
QY 549 gagaaaaacgagtggtctcctcctctgtagtaactgtaagaaaaagcctggagtgacacgaagtgt 608
|||||
Db 2128 gagaaaaacgagtggtctcctcctgtagtaactgtaagaaaaagcctggagtgacacgaagtgt 2187
|||||
QY 609 gcctaccccgagattgagaatgttaagggcactgaggaactcagcaccacag 659
|||||
Db 2188 gcctaccccgagattgagaatgttaagggcactgaggaactcagcaccacag 2238
|||||

Search completed: August 14, 2001, 06:22:14
Job time: 2646 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 05:37:38 ; Search time 80.45 Seconds
(without alignments)
2009.592 Million cell updates/sec

Title: US-09-599-400A-1
Perfect score: 854
Sequence: 1 gadtgagagccatagctgt.....ggcagagcaggaacaatggg 854

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676.6	79.2	2062	1 US-08-050-319B-24	Sequence 24, Appl
2	676.6	79.2	2062	2 US-08-465-982-24	Sequence 24, Appl
3	676.6	79.2	2161	3 US-09-106-038A-1	Sequence 1, Appl
4	676.6	79.2	2175	1 US-08-321-668-1	Sequence 1, Appl
5	676.6	79.2	2175	1 US-08-837-941-1	Sequence 1, Appl
6	676.6	79.2	2175	1 US-08-126-016-1	Sequence 1, Appl
7	651	76.2	6889	1 US-08-286-740-2	Sequence 2, Appl
8	651	76.2	6889	5 PCT-US95-09576-2	Sequence 2, Appl
9	635.8	74.4	6896	2 US-08-627-151A-6	Sequence 6, Appl
10	595.2	69.7	600	1 US-08-050-319B-47	Sequence 47, Appl
11	595.2	69.7	600	2 US-08-465-982-47	Sequence 47, Appl
12	514	60.2	1301	4 US-08-804-166-7	Sequence 7, Appl
13	514	60.2	1301	4 US-08-910-991-7	Sequence 7, Appl
14	506	59.3	1147	4 US-08-804-166-5	Sequence 5, Appl
15	506	59.3	1147	4 US-08-910-991-5	Sequence 5, Appl
16	503	58.9	504	1 US-08-050-319B-56	Sequence 56, Appl
17	503	58.9	504	2 US-08-465-982-56	Sequence 56, Appl
18	501	58.7	501	1 US-08-050-319B-1	Sequence 1, Appl
19	501	58.7	501	2 US-08-465-982-1	Sequence 1, Appl
20	424.4	49.7	1049	4 US-08-804-166-1	Sequence 1, Appl
21	424.4	49.7	1049	4 US-08-910-991-1	Sequence 1, Appl
22	424.4	49.7	1202	4 US-08-804-166-3	Sequence 3, Appl
23	424.4	49.7	1202	4 US-08-910-991-3	Sequence 3, Appl
24	408.8	47.9	1956	2 US-08-762-308-10	Sequence 10, Appl
25	377.8	44.2	477	1 US-08-050-319B-53	Sequence 53, Appl
26	377.8	44.2	477	1 US-08-465-982-53	Sequence 53, Appl
27	372	43.6	372	1 US-08-050-319B-3	Sequence 3, Appl

28	372	43.6	372	2 US-08-465-982-3	Sequence 3, Appl
29	357.2	41.8	474	1 US-08-050-319B-49	Sequence 49, Appl
30	357.2	41.8	474	1 US-08-465-982-49	Sequence 49, Appl
31	312.4	36.6	462	2 US-08-050-319B-51	Sequence 51, Appl
32	312.4	36.6	462	2 US-08-465-982-51	Sequence 51, Appl
33	39.4	4.6	665	1 US-08-322-742-17	Sequence 17, Appl
34	39.2	4.6	1737	1 US-08-202-056-4	Sequence 4, Appl
35	39.2	4.6	1737	1 US-08-076-093A-3	Sequence 3, Appl
36	39.2	4.6	1737	1 US-08-701-265-3	Sequence 3, Appl
37	39.2	4.6	1737	2 US-08-284-586-3	Sequence 3, Appl
38	39.2	4.6	1737	2 US-08-805-478-3	Sequence 3, Appl
39	39.2	4.6	1737	2 US-08-802-627A-3	Sequence 3, Appl
40	39.2	4.6	1737	2 US-08-801-238-3	Sequence 3, Appl
41	39.2	4.6	1737	2 US-08-801-228-3	Sequence 3, Appl
42	39.2	4.6	1737	3 US-09-104-296-3	Sequence 3, Appl
43	39.2	4.6	1737	5 PCT-US94-06380-2	Sequence 2, Appl
44	39	4.6	246240	2 US-08-724-394A-20	Sequence 20, Appl
45	39	4.6	246240	2 US-08-724-394A-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-050-319B-24
; Sequence 24, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
; US-08-050-319B-24

Query Match 79.2%; Score 676.6; DB 1; Length 2062;
Best Local Similarity 95.3%; Pred. No. 8.4e-187;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1 gactgagagccatagctgtctggcagtgagcctctccacagtgccctgacactgctgtgccc 60
Db 130 GAGTGAGAGGCCATAGCTGTGTGGCATGGCCCTCTCCACCGTGCCTGACCTGTCTGTGCC 189
QY 61 gctggctcctgagctgtgtggaatataccctcaggggttattgactggtgcc 120
Db 190 GCTGGTGTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTGTCC 249
QY 121 tcacctaggagagcaggagagagatagtggtgtccccaaggaaatatatccaccc 180
Db 250 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTGCCCAAGGAATATATCCACCC 309
QY 181 tcaataatctgattgtgtgtaccagtgcccaaggaaactactgtacaaatgactg 240
Db 310 TCAATAATTCGATTGTGTGTACCAAGTCCCAAGGAACCTACTGTGTACAAATGACTG 369
QY 241 tcagggccggggcagagatagcagctcagggagtgagagcgtctcctccacgcttc 300
Db 370 TCAGGCCCCGGGCGAGATACGGACTGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTC 429
QY 301 agaaaaccacctcagacactgctcagctgtcctcaaatgcaatgagcctgtcctcaatgg 360
Db 430 AGAAACCACCTCAGACACTGCTCAGCTGCTCCAATGCCGAAGGAATGGTCAAGGT 489
QY 361 ggagatctcttctgacagtgagccgggagacacogtgtgtggtgaggaagaccagta 420
Db 490 GGAGATCTCTCTTGCACAGTGCAGGGACACCGTGTGTGGCTGCAGGAAGAACCACTA 549
QY 421 ccggcattattggagtgaaacacctttccagtgcttcaatgtcagcctctgctcaatgg 480
Db 550 CCGGCATTATTGGAGTGAAACCTTTTCCAGTGTCTCAATTCAGCGCTCTGCCTCAATGG 609
QY 481 gacctgcaactctcctgcccagagagaaacacacogtgtgtggtgaggaagaccagta 540
Db 610 GACCGTGCACTCTCTCTGCAGAGAAACAGACACCGTGTGTGCACTGTGCCACTGTGCA 599
QY 541 ctttctaagagaaacagtggtgtctcctgtagtaactgtaagaaagcctggagtgac 600
Db 670 CTTTCTAAGAGAAACAGTGTGTCTCTGTAGTAAGTGTAAAGAAAGCCTGTGAGTGCAC 729
QY 601 gaagtgtgctcctacccagattgagaatgttaaggagcactgaggaactcaggcaccagtt 660
Db 730 GAAGTTGTGCTCTACCCAGATTGAGAATGTAAAGGGCACTGAGGACTCAGGCACACAGT 789
QY 661 gctgtgccccctggttgcctcctgagcctttccacagtgataagcaggtttttttgtt 720
Db 790 GCTGTGCCCCCTGGTCAATTTCTTTGGTCTTTTGGCTTTTATCCCTCTCTCTTCATTTG 849
QY 721 ttgtttttgtt 731
Db 850 AATGTATCGCT 860

RESULT 2
US-08-465-982-24
; Sequence 24, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
; US-08-465-982-24

Query Match 79.2%; Score 676.6; DB 2; Length 2062;
Best Local Similarity 95.3%; Pred. No. 8.4e-187;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 gactgagagccatagctgtctggcagtgagcctctccacagtgccctgacactgctgtgccc 60
Db 130 GAGTGAGAGGCCATAGCTGTGTGGCATGGCCCTCTCCACCGTGCCTGACCTGTCTGTGCC 189
QY 61 gctggctcctgagctgtgtggaatataccctcaggggttattgactggtgcc 120
Db 190 GCTGGTGTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTGTCC 249
QY 121 tcacctaggagagcaggagagagatagtggtgtccccaaggaaatatatccaccc 180
Db 250 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTGCCCAAGGAATATATCCACCC 309
QY 181 tcaataatctgattgtgtgtaccagtgcccaaggaaactactgtacaaatgactg 240
Db 310 TCAATAATTCGATTGTGTGTACCAAGTGCAGGGACACCGTGTGTGCAAGGAACCACTG 369
QY 241 tcagggccggggcagagatagcagctcagggagtgagagcgtctcctccacgcttc 300
Db 370 TCAGGCCCCGGGCGAGATACGGACTGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTC 429
QY 301 agaaaaccacctcagacactgctcagctgtcctcaaatgcaatgagcctgtcctcaatgg 360
Db 430 AGAAACCACCTCAGACACTGCTCAGCTGCTCCAATGCCGAAGGAATGGTCAAGGT 489
QY 361 ggagatctcttctgacagtgagccgggagacacogtgtgtggtgaggaagaccagta 420
Db 490 GGAGATCTCTCTTGCACAGTGCAGGGACACCGTGTGTGGCTGCAGGAAGAACCACTA 549
QY 421 ccggcattattggagtgaaacacctttccagtgcttcaatgtcagcctctgctcaatgg 480
Db 550 CCGGCATTATTGGAGTGAAACCTTTTCCAGTGTCTCAATTCAGCGCTCTGCCTCAATGG 609
QY 481 gacctgcaactctcctgcccagagagaaacacacogtgtgtggtgaggaagaccagtt 540
Db 610 GACCGTGCACTCTCTCTGCAGAGAAACAGACACCGTGTGTGCACTGTGCCACTGTGCA 600
QY 541 ctttctaagagaaacagtggtgtctcctgtagtaactgtaagaaagcctggagtgac 600
Db 670 CTTTCTAAGAGAAACAGTGTGTCTCTGTAGTAAGTGTAAAGAAAGCCTGTGAGTGCAC 729

QY 601 gaagttgtcctaccacagattgagaatgtttaaggccactgaggactcaggcaccacagtt 660
Db 730 GAAGTTGTGCTACCCAGATGGAATGTTAAGGGCACTGAGGACTCAGGCACACAGT 789
QY 661 gctgtgcccctgttctgctccctgagcctttttcacagtgcataagcagttttttttgt 720
Db 790 GCTGTGCCCCGTGTCATTTCTTGTGCTTGTGCTTTTATCCCTCCCTTCATTTGGTTT 849
QY 721 ttgtttttgtt 731
Db 850 AATGTATCGCT 860
RESULT 3
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowseert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; TELEFAX: (760) 603-3820
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-106-038A-1
Query Match 79.2%; Score 676.6; DB 3; Length 2161;
Best Local Similarity 95.3%; Pred. No. 8.6e-187;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1 gagtggagggccatagctgtctggcattggggcctctccaccgtgctgacctgctgtgcc 60
Db 231 GAGTGAGAGGCCATAGCTGTCTGCGATGGGCTCTCCACCGCTGCTGACCTGCTGCTGCC 290
QY 61 gctgtgtcctgctgagctgtgtgtggaataaccctcaggggttatgtgactggtccc 120
Db 291 GCTGTGCTCCTGAGCTGTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 350
QY 121 tcacctaggggagcaggagagagatagtggtgtccccaagagaaatatatccacc 180
Db 351 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTCGCCCAAGAAATATATCCACCC 410
QY 181 tcaataataatcgtattgtctgctacaaagtcacaaaggaacctactgtacaatgactg 240
Db 411 TCATAAATAATTCGATTGTGCTGTACCAAGTGGCCACAAGAAACCTACTGTACATGACTG 470

QY 241 tcaggcccgggcaggatcacgagtcgaggagtgagagcgttccttaccctcc 300
Db 471 TCCAGGCCCGGGCAGGATACGACTGCAGGGAGTGTAGAGCGGCTCCCTTACCCTTC 530
QY 301 aaaaaaacaccctcagacactgctcagctcccaatgccgaagaaatgggtcaggt 360
Db 531 AGAAAACACCCTCAGACACTGCCCTCAGCTGCTCCAATGCCGAAGAAATGGGTCAAGT 590
QY 361 ggagatctctcttcgacagtgagaccgggacacccgtgtgtggctgagggaagaccagta 420
Db 591 GGAGATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTA 650
QY 421 ccggcattatggagtgaaaaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 651 CCGGCATTATTGGAGTGAACACCTTTTCCAGTGTCTCAATTGCGAGCTCTGCTCAATGG 710
QY 481 gacctgcaacctctcctgcaggagaaacagaaacacccgtgtgcacctgcacctcaagttt 540
Db 711 GACCGTGCACCTCTCTCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAGTTT 770
QY 541 ctttctaagagaaacgagtgctctcctgtagtaactgaaagaaagcctggagtgac 600
Db 771 CTTTCTAAGAGAAACGAGTGTGTCTCTCTGTAGTAAGTAAGAAAGCCTGGAGTGCAC 830
QY 601 gaagttgtcctaccacagattgagaatgtttaaggccactgaggactcaggcaccacagtt 660
Db 831 GAAGTTGTGCTACCCACCATTTGAGGAATGTTAAGGGCACTGAGGACTCAGGCACACAGT 890
QY 661 gctgtgcccctgttctgctccctgagcctttttcacagtgcataagcagttttttgtt 720
Db 891 GCTGTGCCCCGTGTCATTTCTTGTGCTTTTATCCCTCCCTCTCTCTTCATTTGGTTT 950
QY 721 ttgtttttgtt 731
Db 951 AATGTATCGCT 961
RESULT 4
US-08-321-668-1
; Sequence 1, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2175 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 256..1620

US-08-321-668-1

Query Match 79.2%; Score 676.6; DB 1; Length 2175;
Best Local Similarity 95.3%; Pred. No. 8.6e-187;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```
QY 1 gactgagagccatagctgtcgtgcatggccctccaccgtaccctgacctgctgccc 60
Db 231 GAGTGAGAGGCCATAGCTGTGCGATGGGCGCTCTCCACCGTGGCTGACCTGCTGCTGCC 290
QY 61 gctggtgctcctgagctgtgtggtgggaatataccctcaggggttattggactggtccc 120
Db 291 GCTGGTGTCTCTGAGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 350
QY 121 tcacctaggggacagggagagagatagtggtgtgtgtccccaagggaataatataccaccc 180
Db 351 TCACCTAGGGGACAGGAGAGAGAGATAGTGTGTGTCCCAAGGAAATATATCCACCC 410
QY 181 tcaaaataattcattgtgtgtaccaggtcccaaggaacactactgtacaaatgactg 240
Db 411 TCAAAATAATTCTGATTGTGTGTACCAAGTGCCCAAGGAAACCTTGTGTACAAATGACTG 470
QY 241 tcaggccggggcagagatagcagactgagggagtgtgagagcgctccttcaacgcttc 300
Db 471 TCCAGGCCGGGCGAGGATACGGAGTACGGAGTGTGAGAGCGGCTCTTCAACCGCTTC 530
QY 301 agaaaccacctcagacactgctcagctgctccaaatgccgaaggaataatggctcaggt 360
Db 531 AGAAACCACCTCAGACACTGCTCAGCTGCTCCAAATGCCGAAGGAAATGGGTCAAGT 590
QY 361 ggagatctcttgcacagtgaacgggacacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
Db 591 GGAGATCTCTTCTTGCACAGTGGACCGGGGACACCGTGTGTGTGTGTGTGTGTGTGTGT 650
QY 421 cgggcattattgagtgaaacacctttccagtgcttcaattgcaagcctctgctcaatgg 480
Db 651 CCGGCATTATTGGAGTGAAACCTTTTCCAGTGTCTCAATTGACGCTCTGCCCTCAATGG 710
QY 481 gaccgtgacacctcctgccagagagaacacacacggtgtgcaacctgccaatgcaagttt 540
Db 711 GACCGTGACCTCTCTCGCAGGAGAAACACACACCGTGTGTGACCTGTGCCATGAGTTT 770
QY 541 ctttctaaggaagaaacagtggtgtcctcctgtagtaactgttaagaaagcctggagtgac 600
Db 771 CTTCTTAAGGAAGAAACAGTGTGTCTCTGTAGTAACGTAAAGAAAGACCTGGAGTGCAC 830
QY 601 gaagtgtgctcctccacagattgagaatgtaagggcactgaggaactcaggaccacagtt 660
Db 831 GAAGTGTGCTCCTACCCAGATTGAGAAATGTTAAGGGGACACTGAGGACACTCAGGACCA 890
QY 661 gctgtgcccctgttgcgtccctgagcgtttttcacagtgatgataagcagttttttttgt 720
Db 891 GCNGTGGCCCTGGTCATTTCTTGTGCTTGTGCTTTTATCCCTCTCTCTTCATTGTTT 950
QY 721 ttgtttttgtt 731
Db 951 AATGTATCGCT 961.
```

RESULT 5

US-08-837-941-1

Sequence 1, Application US/08837941

Patent No. 5766917

GENERAL INFORMATION:

APPLICANT: WALLACH, David

APPLICANT: BRAKEBUSCH, Cord

APPLICANT: VARFOLOMEYEV, Eugene

APPLICANT: BATKIN, Michael

TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF

TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/837,941

FILING DATE: 28-APR-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/321,668

FILING DATE: 12-OCT-1994

APPLICATION NUMBER: IL 107268

FILING DATE: 12-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: WALLACH=13

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2175 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 256..1620

US-08-837-941-1

Query Match 79.2%; Score 676.6; DB 1; Length 2175;
Best Local Similarity 95.3%; Pred. No. 8.6e-187;
Matches 697; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

```
QY 1 gactgagagccatagctgtcgtgcatggccctccaccgtgacctgacctgctgccc 60
Db 231 GAGTGAGAGGCCATAGCTGTGCGATGGGCGCTCTCCACCGTGGCTGACCTGCTGCTGCC 290
QY 61 gctggtgctcctgagctgtgtggtgggaatataccctcaggggttattggactggtccc 120
Db 291 GCTGTGTCTCTGAGCTGTGTGGGAATATACCCCTCAGGGGTTATTGGACTGGTCCC 350
QY 121 tcacctaggggacagggagagagatagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
Db 351 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 410
QY 181 tcaaaataattcattgtgtgtaccaggtgcccaaggaacactactgtacaaatgactg 240
```

Db	411	TCAAAATAATTGCAATTTGCTGTACCAAGTCCACAAGGAACCTACTTGTACAATGACTG	470
Qy	241	tccaggcccgggcaggatatacgactgcaggagtgtagagcggctccttcacgcgttc	300
Db	471	TCCAGGCCCGGGCAGGATACGGACTGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTC	530
Qy	301	agaaaccacccctcagacactgcctcagctgctccaaatgccgaaggaataatgggtcaggt	360
Db	531	AGAAACACACTCAGACACTGCTCAGCTGCTCCAATGCCAAGGAATAATGGTCAAGT	590
Qy	361	ggagatcctcttgcacagtgcaggagacaccgctgtgtgctgcagaaagaaaccagta	420
Db	591	GGAGATCTCTTCTTGACAGTGCAGCGGACACCGTGTGGCTGCAGGAAGAACCACTA	650
Qy	421	ccggcattatggagtgaaaacctttccagtgctccaattgcagcctctgctcaatgg	480
Db	651	CCGGCATATTGGAGTCAAAACCTTTTCAGTGTCTCAATTGCAGGCTCTGCCCTCAATGG	710
Qy	481	gaccgtgcacctcctgcaggagaaaaacagaaacacctgtgcactgcactgcaggttt	540
Db	711	GACCGTGCACCTCTCCTGCCAGGAGAAACAGAACCCGTGTGCACCTGCCATGCAGGTTT	770
Qy	541	ctttctaagaaaaacagagtgctctcctgtagtaactgtaagaaagcctggagtgcaac	600
Db	771	CTTTCTAAGAGAAAACAGAGTGTCTCTCTGTAGTAAGTCTAAGAAAAGCCTGGAGTGAC	830
Qy	601	gaagttgtgctaccccagattgagaatgttaaggcactgaggactcaggcacacagt	660
Db	831	GAAGTTGTGCTTACCCGAGATTGAGAAATGTTAAGGCATCTAGGACTCAGGCACCAAGT	890
Qy	661	gctgttgcacctggctgcctccctgagocctttttcacagtgcaataagcagtttttttgtt	720
Db	891	GCTGTTGCCCTGGTCATTTCTTTGGTCTTTGCCCTTTATCCCTCCTCTTCATGGTTT	950
Qy	721	tttgttttgtt	731
Db	951	AATGATCGCT	961

RESULT 6

```

US-08-126-016-1
; Sequence 1, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, DAVID
; APPLICANT: NOPHAR, YARON
; APPLICANT: KEMPER, OLIVER
; APPLICANT: ENGELMANN, HARTMUT
; APPLICANT: BRAKEBUSCH, CORD
; APPLICANT: ADERKA, DAN
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
; PROTEIN IN A CELLULAR EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Broadway and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,016
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/625668
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:

```


MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910.991
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804.166
FILING DATE: 20 February 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011.936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 279..1287
US-08-910-991-7

Query Match 60.2%; Score 514; DB 4; Length 1301;
Best Local Similarity 100.0%; Pred. No. 1e-139;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 gatagtgtgtcccccaaggaaataatccaccctcaaaataattcgattgctgtacc 205
Db |||||||
Qy 345 gatagtgtgtgtcccccaaggaaataatccaccctcaaaataattcgattgctgtacc 404
Db |||||||
Qy 206 aagtgtcccaaggaaacaccttctgtacatgactgtccaggcccgaggcaggtacggac 265
Db |||||||
Qy 405 aagtgtcccaaggaaacaccttctgtacatgactgtccaggcccgaggcaggtacggac 464
Db |||||||
Qy 266 tgcaggaggtgtgagagcggtccctccaccgttcagaaaaaacaccctcagacactgcctc 325
Db |||||||
Qy 465 tgcaggaggtgtgagagcggtccctccaccgttcagaaaaaacaccctcagacactgcctc 524
Db |||||||
Qy 326 agctgtcctcaaatgccaaaggaaatgggtcaggtggagatctcttcttgacagtggac 385
Db |||||||
Qy 525 agctgtcctcaaatgccaaaggaaatgggtcaggtggagatctcttcttgacagtggac 584
Db |||||||
Qy 386 cgggacacccgtgtgtggtgtcagggaagaccagtagtccaggcattattggagtgaaacacctt 445
Db |||||||
Qy 585 cgggacacccgtgtgtggtgtcagggaagaccagtagtccaggcattattggagtgaaacacctt 644
Db |||||||
Qy 446 ttccagtgcttcaattgacgctctgcctcaatgggaccgtgcacctctcctgcccaggag 505
Db |||||||
Qy 645 ttccagtgcttcaattgacgctctgcctcaatgggaccgtgcacctctcctgcccaggag 704
Db |||||||
Qy 506 aaacagaaacaccgtgtgcacctgcacgtgttcttcttaagagaaaaacagtggtgtc 565
Db |||||||
Qy 705 aaacagaaacaccgtgtgcacctgcacgtgttcttcttaagagaaaaacagtggtgtc 764
Db |||||||
Qy 566 tccgtgaactgtaaagaaagcctgagtgacagagttgtgctaccacagattgag 625
Db |||||||
Qy 765 tccgtgaactgtaaagaaagcctgagtgacagagttgtgctaccacagattgag 824
Db |||||||
Qy 626 aatgttaagggcactgaggaactcaggccaccag 659
Db |||||||
Qy 825 aatgttaagggcactgaggaactcaggccaccag 858
Db |||||||

RESULT 14
US-08-804-166-5
Sequence 5, Application US/08804166
Patent No. 6193972
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804.166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011.936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1147 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 278..1132
US-08-804-166-5

Query Match 59.3%; Score 506; DB 4; Length 1147;
Best Local Similarity 99.0%; Pred. No. 2e-137;
Matches 509; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 146 gatagtgtgtgtcccccaaggaaataatccaccctcaaaataattcgattgctgtacc 205
Db |||||||
Qy 344 gatagtgtgtgtgtcccccaaggaaataatccaccctcaaaataattcgattgctgtacc 403
Db |||||||
Qy 206 aagtgtcccaaggaaacaccttctgtacatgactgtccaggcccgaggcaggtacggac 265
Db |||||||
Qy 404 aagtgtcccaaggaaacaccttctgtacatgactgtccaggcccgaggcaggtacggac 463
Db |||||||
Qy 266 tgcaggaggtgtgagagcggtccctccaccgttcagaaaaaacaccctcagacactgcctc 325
Db |||||||
Qy 464 tgcaggaggtgtgagagcggtccctccaccgttcagaaaaaacaccctcagacactgcctc 523
Db |||||||
Qy 326 agctgtcctcaaatgccaaaggaaatgggtcaggtggagatctcttcttgacagtggac 385
Db |||||||
Qy 524 agctgtcctcaaatgccaaaggaaatgggtcaggtggagatctcttcttgacagtggac 583
Db |||||||
Qy 386 cgggacacccgtgtgtggtgtcagggaagaccagtagtaccgtgagtgaaacacctt 445
Db |||||||

Db 584 CGGACACCGTGTGGTGTGAGGAGAACACAGTACCGGCAATTATTGGAGTGAACACCTT 643
QY 446 tccagtgcttcaattgagcctctgctcaatgagacgtgacacctctcctgccaaggag 505
Db 644 TTCAGTGTCTCAATTGACCTCTGCTCTCAATGGACCGTGCACCTCTCCCTGTCAGGAG 703
QY 506 aaacagaacacgtgtgacacgtgacacgtgacacgttcttcttaagagaaacagagtgtc 565
Db 704 AAACAGAACACCGTGTGACCTGTGACCTGACCTGAGTCTTCTTAAAGAGAAACAGTGTGC 763
QY 566 tccgtagtaactgtaagaaacgtgagtgacagaaagtgtgctacccagattgag 625
Db 764 TCCTGTAGTAAGTGAAGAAAGCCCTGGAGTGCAGAACTTGTCCCTACCCAGATTGAG 823
QY 626 aatgttaaggacactgagactcagggcaccacag 659
Db 824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 857

RESULT 15

US-08-910-991-5
; Sequence 5, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,991
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE: 20 February 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: CAMPBELL-2B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1147 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 278..1132
US-08-910-991-5

Query Match 59.3%; Score 506; DB 4; Length 1147;

Best Local Similarity 99.0%; Pred. No. 2e-137;
Matches 509; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 146 gatagtggtgtccccaagaaaaatatatccaccctcaaaaataattgattgtctgtacc 205
Db 344 GATAGTGTGTGTCCCAAGGAAAATATATCCACCCTCAAAAATAATTGATTTGCTGTACC 403
QY 206 aagtgcacacaaagaaacctactgtacaatgactgtccagcccggggagagatacggac 265
Db 404 AAGTGCACAAAAGAAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACCGAC 463
QY 266 tgacggagtgtagagcggcctctcacgcgttcagaaaaaccacctcagacactgcctc 325
Db 464 TGCAGGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAAAACCACTCAGACACTGCCTC 523
QY 326 agtgtctccaaatgccgaagaaatgggtcagtgagagatctcttcttcacagtgac 385
Db 524 AGTGTCTCCAAATGCCGAAAGAAATGGGTGAGGAGATCTCTTCTTGACAGATGGAC 583
QY 386 cgggacacccgtgtgtgctgcaggaagaaccagTaccggcattattggagtgaacacct 445
Db 584 CGGACACCGTGTGTGGCTGCAGGAAGAACACAGTACCGGCATTATTGGAGTGAAACCTT 643
QY 446 tccagtgcttcaattgagcctctgctcctcaatgggaccgtgcacctctcctgcaggag 505
Db 644 TTCAGTGTCTCAATTGACCTCTGCTCAATGGACCGTGCACCTCTCCTGTGAGGAG 703
QY 506 aaacagaacacccgtgtgacacgtgacacgtgacacgttcttcttaagagaaacagagtgtc 565
Db 704 AAACAGAACACCGTGTGACCTGTGACCTGCAATGCAGGTTCTTCTTAAGAGAAAAAGAGTGTCTC 763
QY 566 tctgtagtaactgtaagaaacgtgagtgacagagtgtgctaccctaccagattgag 625
Db 764 TCCTGTAGTAAGTGAAGAAAGCCCTGGAGTGCAGAACTTGTCCCTACCCAGATTGAG 823
QY 626 aatgttaaggacactgagactcagggcaccacag 659
Db 824 AATGTTAAGGGCACTGAGGACTCAGGCACCACAG 857

Search completed: August 14, 2001, 06:20:01
Job time: 2543 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 14, 2001, 05:36:43 ; Search time 1170.31 Seconds
(without alignments)
6897.947 Million cell updates/sec

Title: US-09-599-400A-1
Perfect score: 854
Sequence: 1 gagtgcagagccatagctgt.....ggcgagcgcggaacaatggg 854

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1:	gb_est1:
2:	gb_est2:
3:	gb_est3:
4:	gb_est4:
5:	gb_est5:
6:	gb_est6:
7:	gb_est7:
8:	gb_est8:
9:	gb_est9:
10:	gb_est10:
11:	gb_est11:
12:	gb_est12:
13:	gb_est13:
14:	gb_est14:
15:	gb_est15:
16:	gb_est16:
17:	gb_est17:
18:	gb_est18:
19:	gb_est19:
20:	gb_est20:
21:	gb_est21:
22:	gb_est22:
23:	gb_est23:
24:	gb_est24:
25:	gb_est25:
26:	gb_est26:
27:	gb_est27:
28:	gb_est28:
29:	gb_est29:
30:	gb_est30:
31:	gb_est31:
32:	gb_est32:
33:	gb_est33:
34:	gb_est34:
35:	gb_est35:
36:	gb_est36:
37:	gb_est37:
38:	gb_est38:
39:	gb_est39:
40:	gb_est40:
41:	gb_est41:
42:	gb_est42:
43:	gb_est43:

44: em_esthum10:*

45: em_esthum11:*

46: em_esthum12:*

47: em_esthum13:*

48: em_esthum14:*

49: em_esthum15:*

50: em_esthum16:*

51: em_esthum17:*

52: em_esthum18:*

53: em_esthum19:*

54: em_esthum20:*

55: em_esthum21:*

56: em_esthum22:*

57: em_esthum23:*

58: em_esthum24:*

59: em_esthum25:*

60: em_esthum26:*

61: em_esthum27:*

62: em_esthum28:*

63: em_estin1:*

64: em_estin2:*

65: em_estin3:*

66: em_estin4:*

67: em_estin5:*

68: em_estom1:*

69: em_estom2:*

70: em_estov1:*

71: em_estov2:*

72: em_estpl1:*

73: em_estpl2:*

74: em_estpl3:*

75: em_estpl4:*

76: em_estpl5:*

77: em_estpl6:*

78: em_estpl7:*

79: em_estpl8:*

80: em_estpl9:*

81: em_estpl10:*

82: em_estro1:*

83: em_estro2:*

84: em_estro3:*

85: em_estro4:*

86: em_estro5:*

87: em_estro6:*

88: em_estro7:*

89: em_estro8:*

90: em_estro9:*

91: em_estro10:*

92: em_estro11:*

93: em_estro12:*

94: em_estro13:*

95: em_estro14:*

96: em_estro15:*

97: em_estro16:*

98: em_estro17:*

99: em_estro18:*

100: em_estro19:*

101: em_estro20:*

102: gb_est25:*

103: gb_est26:*

104: gb_est27:*

105: gb_est28:*

106: gb_est29:*

107: gb_est30:*

108: gb_est31:*

109: gb_est32:*

110: gb_est41:*

111: gb_est42:*

112: gb_est43:*

113: gb_est44:*

114: gb_est45:*

115: gb_est46:*

116: gb_est47:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: gb_est121:*
191: gb_est122:*
192: gb_est123:*
193: gb_est124:*
194: gb_est125:*
195: gb_est126:*
196: gb_est127:*
197: gb_est128:*
198: gb_est129:*
199: gb_est130:*
200: gb_est131:*
201: gb_est132:*
202: gb_est133:*
203: gb_est134:*
204: gb_est135:*
205: gb_est136:*
206: gb_est137:*
207: gb_est138:*
208: gb_est139:*
209: gb_est140:*
210: gb_est141:*
211: gb_est142:*
212: gb_est143:*
213: gb_est144:*
214: gb_est145:*
215: gb_est146:*
216: gb_est147:*
217: gb_est148:*
218: gb_est149:*
219: gb_est150:*
220: gb_est151:*
221: gb_est152:*
222: gb_est153:*
223: gb_est154:*
224: gb_est155:*
225: gb_est156:*
226: gb_est157:*
227: gb_est158:*
228: gb_est159:*
229: gb_est160:*
230: gb_est161:*
231: gb_est162:*
232: gb_est163:*
233: gb_est164:*
234: gb_est165:*
235: gb_est166:*
236: gb_est167:*
237: gb_est168:*
238: gb_est169:*
239: gb_est170:*
240: gb_est171:*
241: gb_est172:*
242: gb_est173:*
243: gb_est174:*
244: gb_est175:*
245: gb_est176:*
246: gb_est177:*
247: gb_est178:*
248: gb_est179:*
249: gb_est180:*
250: gb_est181:*
251: gb_est182:*
252: gb_est183:*
253: gb_est184:*
254: gb_est185:*
255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	675	79.0	957	106	AL559050	AL559050	AL559050
2	661.8	77.5	837	105	AL522989	AL522989	AL522989
3	660	77.3	761	108	AU131978	AU131978	AU131978
4	659	77.2	975	106	AL577008	AL577008	AL577008
5	650.8	76.2	942	105	AL529836	AL529836	AL529836
6	643.6	75.4	974	174	BG180101	602329676	BG180101 602329676
7	587.4	68.8	845	107	AU125021	AU125021	AU125021
8	583.2	68.3	767	108	AU142156	AU142156	AU142156
9	582.4	68.2	859	107	AU124446	AU124446	AU124446
10	564.4	66.1	971	141	BE876920	601488490	BE876920 601488490
11	564	66.0	772	107	AU137990	AU137990	AU137990
12	550.2	64.4	817	107	AU125680	AU125680	AU125680
13	529.8	62.0	706	107	AU124156	AU124156	AU124156
14	513.6	60.1	802	108	AU142163	AU142163	AU142163
15	513.2	60.1	805	107	AU125694	AU125694	AU125694
16	512.4	60.0	712	137	BE549214	601078765	BE549214 601078765
17	512.2	60.0	834	107	AU126303	AU126303	AU126303
18	510.2	59.7	788	107	AU124519	AU124519	AU124519
19	499.6	58.5	942	141	BE869492	601446157	BE869492 601446157
20	495	58.0	969	141	BE871809	601448388	BE871809 601448388
21	476	55.7	534	170	AI186844	q36e12.s	AI186844 q36e12.s
22	461.2	54.0	491	170	BF839822	RC3-HT023	BF839822 RC3-HT023
23	461	54.0	742	107	AU125646	AU125646	AU125646
24	457	53.5	934	175	BG257904	602379540	BG257904 602379540
25	449	52.6	475	139	BE710028	IL3-HT061	BE710028 IL3-HT061
26	433.8	50.8	624	165	BE295225	601175209	BE295225 601175209
27	432.4	50.6	484	169	BF807089	IL5-C1014	BF807089 IL5-C1014
28	414.2	48.5	612	108	AU139183	AU139183	AU139183
29	410	48.0	652	108	AU137288	AU137288	AU137288
30	402.4	47.1	706	141	BE909651	601501658	BE909651 601501658
31	400	46.8	578	168	BF724891	601886717	BF724891 601886717
32	399.8	45.6	926	146	BF303970	601886717	BF303970 601886717
33	389.4	45.6	779	16	AI119338	uf03d04.y	AI119338 uf03d04.y
34	386	45.2	539	141	BE907366	601500087	BE907366 601500087
35	385.6	45.2	415	172	BG001080	QV1-GN020	BG001080 QV1-GN020
36	383.8	44.9	593	108	AU139934	AU139934	AU139934
37	377.4	44.2	658	150	BF528949	602041534	BF528949 602041534
38	376.2	44.1	686	147	BF309089	601890501	BF309089 601890501
39	374	43.8	948	146	BF303965	601886710	BF303965 601886710
40	372.8	43.7	662	107	AU127116	AU127116	AU127116
41	358.2	41.9	416	139	BE693950	MR4-BT059	BE693950 MR4-BT059
42	354	41.5	504	169	BF742282	RC1-BTN04	BF742282 RC1-BTN04
43	350.4	41.0	984	145	BF164835	601777753	BF164835 601777753
44	350	41.0	761	175	BG282718	602406578	BG282718 602406578
45	332.6	38.9	343	170	BF837635	QV3-HT101	BF837635 QV3-HT101

ALIGNMENTS

RESULT 1
 Locus AL559050 957 bp mRNA EST 16-FEB-2001
 DEFINITION AL559050 LTI_NFL008.TC2 Homo sapiens cDNA clone CS0DJ010YB05 5
 prime, mRNA sequence.

ACCESSION AL559050
 VERSION AL559050.1 GI:12904166
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 957)
 AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1..957
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DJ010YB05"
 /clone_lib="LTI_NFL008_TC2"
 /sex="male"
 /tissue_type="T cells from T cell leukemia"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 222 a 262 c 252 g 220 t 1 others
 ORIGIN

Query Match 79.0%; Score 675; DB 106; Length 957;
 Best Local Similarity 95.2%; Pred. No. 4.2e-171;
 Matches 696; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 gagtgaagaccatagctgtctgcatggggcctccaccctgctgacctgctgcc 60
 DB 168 GAGTGAGAGGCATAGCTGTGTCATGGGCTCTCCACCGTGCCTGCTGCTGCC 227
 QY 61 gctggtctcctgagctgtgtgggaataaccctcaggggttattggactgtccc 120
 DB 228 ACTGCTGCTCTGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 287
 QY 121 tcacttagggagacaggagagagatagtggtgtcccaagaaataatataccacc 180
 DB 288 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTCCTCCCAAGGAAATATATCCACC 347
 QY 181 tcaataaattcgtattgtgtacacagtgccacaaagaaacctactgtacaatgactg 240
 DB 348 TCAAAATAATTCGATTTGCTGTACCAAGTCGCACAAAGAACCTACTTGTACAATGACTG 407
 QY 241 tccaggccggggcagatagacgactgcaggagtgtagagcggtcctcaccgcttc 300
 DB 408 TCCAGGCGCGGGCAGGATACGGACTGCAGGAGTGTGAGAGCGGCTCTTTCACCGCTTC 467
 QY 301 agaaaaccctcagacactgcctcagctgtccaaatgccaaagaaatgggtcaggt 360
 DB 468 AGAAACCACTCAGACACTGCCCTCAGCTGTCTCAAAATGCCGAAGGAATGGGTCAAGT 527
 QY 361 ggagatctcttctgcagctggaccgggacacccgtgtgtgctgcaggaagaccagta 420
 DB 528 GGAGATCTCTTTCGACAGTGGACCGGGACACCGCTGTGTGGCTGCAGAGAACCACTA 587
 QY 421 ccggcattattggagtgaaaacctttccagtgcttcaattgcagcctcctcctcaatgg 480
 DB 588 CCGCATATTGGAGTGAACACCTTTTCCAGTGTCTCAATTCAGCCCTCTGCTCAATGG 647
 QY 481 gaccgtcacctctcctgcaggagagaaacagacacccgtgtgcacctgcacgtgaggtt 540
 DB 648 GACCGTCACCTCTCTCCGCCAGGAGAAACAGAACACCCGTGTGCACCTCCCATGCAAGT 707
 QY 541 cttcttaagagaaacagtgctcctctagtaactgttaagaaagcctggagtgacac 600
 DB 708 CTTTCTAAGAGAAACAGTGTGTCTCTGTAGTAACCTGTAGAAAGCCCTGGAGTGAC 767
 QY 601 gaattgtgctacccagattgagaatgttaaggggcactgaggactcaggcaccacagt 660
 DB 768 GAAGTTGTGCTACCCAGATTGAGATGTTAAGGGCACTGAGGACTCAGGACCACTAGT 827

```

Qy 661 gctttgcccctggttgcctcagccttttttccacagtgcataagcagttttttttttt 720
Db 828 GCTGTGCCCCCTGGTCATTTTCCTTGGTCTTTGCTTTTATCCCTCCCTCTTCATTGGTTT 887
Qy 721 ttgtttttgt 731
Db 888 AATGATCGCT 898

RESULT 2
AL522989 AL522989 837 bp mRNA EST 13-FEB-2001
LOCUS AL522989 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB009YP14 5
DEFINITION prime, mRNA sequence.
ACCESSION AL522989
VERSION AL522989.1 GI:12786482
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 837)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 837
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DB009YP14"
/clone_lib="LTI_NFL004_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 199 a 231 c 229 g 177 t 1 others
ORIGIN

Query Match 77.5%; Score 661.8; DB 105; Length 837;
Best Local Similarity 99.7%; Pred. No. 1.5e-167;
Matches 663; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 gagtggaggccatagctgtctggtggaataaccctcaggggtattggactggtccc 60
Db 173 GAGTGAGAGGCCATAGCTGTGGATGGGCTCCACCGTGCCTGACCTGCTGCTGCC 232
Qy 61 gctggtcctcagactgttgggtgggaataaccctcaggggtattggactggtccc 120
Db 233 ACTGCTCTCTGGAGCTGTGGTGGGAATATACCCTCCAGGGGTATTGGACTGGTCCC 292
Qy 121 tcacctgggacaggaggagagatagtggtgtctccccaaggaataatatccaccc 180
Db 293 TCACCTAGGGACAGGGAGAGAGATAGTGTGTGTCCTCCCAAGGAARATATATCCACC 352
Qy 101 tcaaaataattcgtattgtgtaccagtgcacaaagaaacctactgtacaatgactg 240
Db 353 TCAAAATAATTCTGATTCTGTACCAAGTGCCACAAAGAACTACTTGTACAATGACTG 412
Qy 241 tccaggccggggcaggatcagactgcagggagtgtagagcggtctcttcaccgcttc 300

```

```

Db 413 TCAGGCCCCGGGCGAGATACGGACTGCAGGGAGTGTGAGAGCGCTCTTCACCGCTTC 472
Qy 301 aaaaaaccacctcagacactgcctcagctgctccaaatgccaaagaaatgggtcaggt 360
Db 473 AGAAAACCACTCAGACACTGCCTCAGCTCAGCTCCAAATGCCGAAGAAATGGTCAAGT 532
Qy 361 ggagatctctcttgcacagtgcacccgggacaccgtgtgtggctgcagggaacacagta 420
Db 533 GGAGATCTCTTCTTGCACAGTGGAGCCGGGACACCGTGTGTGGCTGCAGGAAGAACAGTA 592
Qy 421 ccggcattattggagtgaaaaaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 593 CCGGCATTATTGGAGTGAAAAACCTTTTCCAGTGTCTTCAATTGCAGCCCTCTGCCTCAATGG 652
Qy 481 gaccgtgcacctctctgcaggagaaacagacacccgtgtgcacctgacctcagctttt 540
Db 653 GACCGTGCACCTCTCTCTGCAGGAGAAACAGAACCCGTGTGCACCTGCCATGCAGTTT 712
Qy 541 ctttctaaagaaaaacgagtgtgtctcctctagtaactgtaaaaaagcctggagtgctac 600
Db 713 CTTTCTAAGAGAAAACGAGTGTCTCTCTGTACTGTAAAGAAAGCCTGGAGTGCAC 772
Qy 601 gaagttgtcctaccaccagattgagaatgttaagggcactgaggaactcagccaccacgt 660
Db 773 GAAGTTGTGCTACCCAGATTGAGAATGTTAAGGGCACTGAGGACTCAGGCACCCACAGT 832
Qy 661 gctgt 665
Db 833 GCTGT 837

RESULT 3
AL521978 AL521978 761 bp mRNA EST 24-OCT-2000
LOCUS AL521978 NT2RP3 Homo sapiens cDNA clone NT2RP3003570 5', mRNA
DEFINITION sequence.
ACCESSION AL521978.1 GI:10992332
VERSION AL521978
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 761)
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isogai, T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. .761
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP3003570"
/clone_lib="NT2RP3"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT 178 a 199 c 201 g 179 t 4 others
ORIGIN

```

```

BP 191 91006 EVRY cedex - France
Email: segrif@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .975
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1082YA01"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
231 a 258 c 221 t 6 others
BASE COUNT
ORIGIN

```

Query Match	77.3%	Score 660;	DB 108;	Length 761;
Best Local Similarity	98.1%	Pred. No. 4.4e-167;		
Matches 666;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps
Oy	1	gagtgagaggccatagctgctcgtgcatggccctccacgcgtgcctgacctgctgctgcc	60	
Db	37	GAGTGAGAGGCCATGAGTGTGTCATGGCCCTCTCACCGTGCCCTGACCTGCTGCTGCC	96	
Oy	61	gctggtgctcctgagctgttggtgggaatatataccctcagggttatggactggtccc	120	
Db	97	ACTGGTGCTCCTGAGCTGTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGCTGCC	156	
Oy	121	tcacctaggggacaggagagagagatagtgtgtgtccccaaggaaaaatatataccacc	180	
Db	157	TCACCTAGGGGACAGGGAGAGAGAGATAGTGTGTGTCCCAAGGAAAATATATCCACCC	216	
Oy	181	tcaaaataattcgtattgctgtaccaggtcccaagaagaacctactgtataaatacgtg	240	
Db	217	TCAAAATAATTTCGATTGTGTGTACCAAGTGCCCAAGGAACCTACTGTACAAATGACTG	276	
Oy	241	tccaggccggggcaggatcacggaactcaggaggtgtgagagcggtccttcaccgccttc	300	
Db	277	TCCAGGCCCGGGCAGGATACGGACTCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTC	336	
Oy	301	agaaaacacctcagacactgctcctcagctgtctccaaatgccgaaaagaaatgggtcaggt	360	
Db	337	AGAAAACACCTCAGACACTGCCTCAGCTGTCTCCAAATGCCAAGAGAAATGGGTCAAGT	396	
Oy	361	ggagatcctcttctgacagtggaccggggacacggtgtgtgctgcaggaagaaccagta	420	
Db	397	GGAGATCTCTTCTTGACAGTGGACCGGGACACCGTGTGTGGCTGCAGGAAGAACCACTA	456	
Oy	421	ccggcattattggagtgaaaacacctttccagtgctctcaattgcagcctctgcctcaatgg	480	
Db	457	CCGGCATATTGGAGTGAAAACCTTTTCCAGTGCTCTCAATTGGCAGGCTCTGCTCAATGG	516	
Oy	481	gaccgtgcacctctcctgccaggagaaacagaacacogtgtgcacctgcaatgcaggttt	540	
Db	517	GACCGTGACACTCTCTCTGCCAGGAGAAACAGACACCGTGTGCACCTGCCATGCAGGTTT	576	
Oy	541	ctttctaagaaaaaacagagtgtctcctctagttaactgtaaagaaagcctggagtgcaac	600	
Db	577	CTTTCTAAGAAAAACAGAGTGTGTCTNCTGTAGTAACTGTAAAGAAAGCCTTGAGTGCA	636	
Oy	601	gaagttgtgcctacccagattgagaatgttaaggggcaactgaggactcaggcaccacagt	660	
Db	637	GAAGTTGTGCTACCCAGATTGAGATGTTTAANGGCATGAGGACTCAGGCACCAACAAT	696	
Oy	661	gctgttgccctggttcgt	679	
Db	697	GCTTGTGGCCCTGCNCAT	715	

RESULT	4				
AL5777008					
LOCUS					
DEFINITION	AL5777008 LTI_NFL006_P12	975 bp	EST	16-FEB-2001	
	prime, mRNA sequence.				
ACCESSION	AL5777008				
VERSION	AL5777008.1	GI:12939716			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 975)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				

```

Db 891 TGCTGTTGCCCTGGTCAATTTCTTTGGTCTTTGCC 925

RESULT 5
AL529836 942 bp mRNA EST 13-FEB-2001
LOCUS LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD005YP05 5
DEFINITION prime, mRNA sequence.
ACCESSION AL529836
VERSION AL529836.1 GI:12793329.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 942)
L1.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..942
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD005YP05"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 208 a 259 c 248 g 224 t 3 others
ORIGIN

Query Match 76.2%; Score 650.8; DB 106; Length 942;
Best Local Similarity 94.7%; Pred. No. 1.4e-164;
Matches 693; Conservative 2; Mismatches 35; Indels 2; Gaps 2;

QY 1 gactgagagccatagctgtctggcatggcctctccaccgtgctacctgctgtgcc 60
|||||
Db 209 GAGTGAGAGCCATAGCTGTGTCATGGGCTCTCCACCGTGCCTGACCTGCTGCC 268
|||||
QY 61 gctgggtgctctgagctgtgtgggaatataccctcaggggtatttgactggtccc 120
|||||
Db 269 GCTGTGCTCTCGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGACGTGCC 328
|||||
QY 121 tcacctaggggacaggagagagatgtgtgtgtcccaaggaaatatatccacc 180
|||||
Db 329 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTCCCAAGGAAATATATCCACC 388
|||||
QY 181 tcaataaattcattgtgtgtaccagtgcccaaggaaacctactgttacaatgactg 240
|||||
Db 389 TCAAAATAATTTCGATTGCTGTACCAAGTCCCAAGGAACCTACTGTACAAATGACTG 448
|||||
QY 241 tcagggccgggacagatcacgactgcaggagtgtgagcggtccctccaccgttc 300
|||||
Db 449 TCCAGGCCCGGGCAGATACGACTCTCAGGGAGTGTGAGACGGCTTCCTTCACCGGTC 508
|||||
QY 301 agaaaaccacctcagacactgcctcagctgtcccaaatgccgaagaaatgggtcaggt 360
|||||
Db 509 AGAAACCACTCAGACACTGCCTCAGCTGCTCCAAATGCCGAAGGAATGGTCAGGT 568
|||||

```

```

QY 361 ggagatctctttgacagtgacccgggacacccgtgtgtgtggtgcaggaagaacagta 420
|||||
Db 569 GGAGATCTCTTCTTGCACAGTGGACCGGACACCCGCTGTGTGTGCTGCAGGAACAACAGTA 628
|||||
QY 421 ccgscattattggagtgaaaaaccttttccagtgcttcaattgacgacctctgctcaatgg 480
|||||
Db 629 CCGCATTTATTGGAGTGAAAACTTTTCCAGTGCTTCAATTGACAGCTCTGCCTCAATGG 688
|||||
QY 481 gaccgtgcacctctcctccagagaaacacacccgtgtgcacctgcacgtgcacgtgcaggt 539
|||||
Db 689 GACCGTGACCTCTCCTCCAGGAGAAACACCCGCTGTGCACCTGCCATGCGAGGTTT 748
|||||
QY 540 tcttttaagagaaaacagtggtgtctcctgttagtaactgttaagaaaagcctggagtgca 599
|||||
Db 749 TCTTCTTAAGAGAAACAGAGTGTCTCTCTGTAGTAAGTAAGADAAGCCTGGAGTGCA 808
|||||
QY 600 cgaagttgtgctaccacccagattgagaatgttaaggagcactgagcactcagcagcacag 659
|||||
Db 809 CG-AGTTGTGCTTACCCAGATTGAGAAATGTAAGGGCACTGAGGACTCAGGCACACAG 867
|||||
QY 660 tgcgtgcccctggtgtccctgagcctttttcacagtgcatagcagttttttgt 719
|||||
Db 868 TGCTGTGCCCTGGTCAATTTCTTTGGTCTGTGCTTTATMCTCTCTTCATGTTT 927
|||||
QY 720 tttgtttttgt 731
|||||
Db 928 TAATGTATCGCT 939
|||||

RESULT 6
BG180101 974 bp mRNA EST 06-FEB-2001
LOCUS 602325676F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5',
DEFINITION mRNA sequence.
ACCESSION BG180101
VERSION BG180101.1 GI:12686804
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 974)
NIH-MGC http://mhc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10185 row: g column: 20
High quality sequence stop: 657.
FEATURES
Location/Qualifiers
1..974
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4431019"
/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: prostate; Vector: pCMV-SPORT6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 259 a 265 c 265 g 185 t
ORIGIN

```

Unpublished (2000)
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3951
 Fax: 81-438-52-3952
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES
 source Location/Qualifiers
 1. .845
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="NT2RM4000896"
 /clone_lib="NT2RM4"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /note="Vector: PME18SFL3; mRNA from uninduced NT2 neuronal
 precursor cells"

BASE COUNT 202 a 232 c 226 g 182 t 3 others
 ORIGIN

Query Match 68.8%; Score 587.4; DB 107; Length 845;
 Best Local Similarity 96.3%; Pred. No. 1.7e-147;
 Matches 632; Conservative 0; Mismatches 19; Indels 5; Gaps 3;

Qy 1 gagtgaaggccatagctgtctggcatgggcctctcaacgtgctgacctgctgctgcc 60
 |||||
 Db 195 GAGTGAGAGGCCATAGCTGTGTCATGGGGCTCTCCACCGTGGCTGACCTGCTGCTGCC 254
 |||||
 Qy 61 gctggtcctcgtgagctgttggtggaataatccctcagggttattgacaggctcc 120
 |||||
 Db 255 ACTGGTCTCTGTGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGTGACATGGTCCC 314
 |||||
 Qy 121 tcacctgaggagcaggagagagatagtgtgtcccaaggaaatatatccaccc 180
 |||||
 Db 315 TCACCTAGGGGGCAGGGAGAAGAGAGATAGTGTGTGCCCAAGGAAATATATCCACCC 374
 |||||
 Qy 181 tcaaaaataattcgtattgctgtaccaagtgccacaaggaaacctacttgtacaatgactg 240
 |||||
 Db 375 TCAAAATAATTCGATTTCGTGTACCAAGTGCACAAAGGAACCTACTTGTGTACAATGACTG 434
 |||||
 Qy 241 tcagggccggggcagatcacgagactcaggaggtgtgagcggtcctctcacgcttc 300
 |||||
 Db 435 TCCAGGCCCGGGGCGAGATACGGACTTCAGGGAGTGTGAGAGCGGCTCTTTCACCGCTTC 494
 |||||
 Qy 301 agaaaaccactcagacactgcctcagctgtcccaatgccgaaaggaaatgggtcaggt 360
 |||||

Unpublished (2000)
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3951
 Fax: 81-438-52-3952
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
 Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES
 source Location/Qualifiers
 1. 845
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="NT2RM4000896"
 /clone_lib="NT2RM4"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
 precursor cells"

BASE COUNT 202 a 232 c 226 g 182 t 3 others
 ORIGIN

Query Match 68.88; Score 587.4; DB 107; Length 845;
 Best Local Similarity 96.3%; Pred. No. 1.7e-147;
 Matches 632; Conservative 0; Mismatches 19; Indels 5; Gaps 3;

QY 1 gqgtgagagccatagctgtctggcatgggctctccacgtgctgacctgctgctgctgcc 60
 |||||
 Db 195 GAGTGAGAGGCCATAGCTGCTGGCATGGGGCTCTCCACGTGGCTGACCTGCTGCTGCC 254
 |||||

QY 61 gctgtgtctctgagctgttgggggaataataccctcaggggtatttgactggtgcc 120
 |||||
 Db 255 ACTGGTGTCTCTGAGCTGTGGTGGGAATATACCCCTCAGGGGTATTGACATGGTGCCC 314
 |||||

QY 121 tcaactggggacaggagagagatagtggtgtccccaagaaataataccacc 180
 |||||
 Db 315 TCACCTAGGGGGCAGGGAGAGAGATAGTGTGTGTGCCCAAGGAAATATATCCACCC 374
 |||||

QY 181 tcaaaataattcattgtgtaccagtgccaaagtcacaaaggaacctactgtacaatgactg 240
 |||||
 Db 375 TCAAAATAATTTCGATTGTGTACCAAGTGCCACAAAGGAACCTACTTGTACAATGACTG 434
 |||||

QY 241 tcagggccggggcaggatcacgagctcaggagtgtagagcggtctctccacgcttc 300
 |||||
 Db 435 TCCAGGCCCGGGGACGATACCGACTCAGGGAGTGTGAGACGGCTCTTTCACCGCTTC 494
 |||||

QY 301 agaaacccactcagacactgcctcagctgctccaaatgccgaagaaatgggtcaggt 360
 |||||
 Db 495 AGAAACCACTCAGACACTGCCTCAGCTGCTCCAATGCCGAAAGGAATGGGTTCAGGT 554
 |||||

QY 361 ggagatctcttctgcacagtggaccgggacaccggtgtgtggtgcaggaagaaccagta 420
 |||||
 Db 555 GGAGATCTCTTTCACAGTGGACCGCGGACACCGTGTGTGGCTGCAGGAAGAACCCAGTA 614
 |||||

QY 421 ccggcatattggagtgaaacactttccagtgcttcaattgagacctctgcctcaatgg 480
 |||||
 Db 615 CCGGCATATTGGAGTGAACAACCTTTTCCAGTGTCTCAATTTGACAGCCTCTGCCCTCAATGG 674
 |||||

QY 481 gacgtgcacctctctgcagagaaacagacacgctgacacctgcacatgcaggttt 540
 |||||
 Db 675 GACCGTGCACCTCTCCCTGCGAGGAGAACACACCGTGTGCACCTGCCATGACGGTTT 734
 |||||

QY 541 ctttctaagaaacacgagtgtgtctcctgtagtaactgtaagaaacgcttgcaggtgcac 600
 |||||
 Db 735 CTTTCTAAGAAACCA- TGTGTCTNCTGTAGTAACTGTAAAGAAAGCCT- GAATGCAC 792
 |||||

QY 601 gaagttgtcctaccccgatttgagaattgtaaggggcactgaggactcaggcaaca 656
 |||||
 Db 793 GAAGTTGTGCTACCC- - - ANATTGAAATGTTAAGGCACTGAGGACTAGCNCACCA 845
 |||||

```

RESULT 8
LOCUS AU142156 767 bp mRNA EST 25-OCT-2000
DEFINITION AU142156 THYR1 Homo sapiens cDNA clone THYR1001863 5', mRNA
sequence.
ACCESSION AU142156
VERSION AU142156.1 GI:11003677
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source Location/Qualifiers
1..767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="THYR1001863"
/clone_lib="THYR1"
/tissue_type="thyroid gland"
/notes="Vector: pME18SFL3"
BASE COUNT 183 a 211 c 210 g 160 t 3 others
ORIGIN
Query Match 68.3%; Score 583.2; DB 108; Length 767;
Best Local Similarity 98.8%; Pred. No. 2.2e-146;
Matches 596; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
Qy 1 gagttagagccatagctgtgtgcatgggctctccaccgtgctgacctgctgctgctgcc 60
Db 166 GAGTGAGAGCCATAGCTGTCTGGCATGGGCTCTCCACCGCTGCTGACCTGCTGCC 225
Qy 61 gctggtctcctgagctgtgtggtggaataataccctcagggttattgactggtccc 120
Db 226 GCTGTGCTCTCTGAGCTGTGTGGTGGGAATATACCCCTCAGGGGTTATTGGACTGTC 285
Qy 121 tcacctaggacaggagagagatagtggtgtccccaaggaataatataccacc 180
Db 286 TCACCTAGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCC 345
Qy 181 tcaataataattcgtattgcttaccagtgcacaaaggaacctacttgtacaatgactg 240
Db 346 TCAAAATAATTCGATTGCTGTACCAAGTGCCACAAAGGAACCTACTGTACATGACTG 405
Qy 241 tcaagcccgccgggagagatacagagactgagggagtgtgagcggtctctcaaccgttc 300
Db 406 TCCAGGCCCGGGGAGGATACGAGCTGCTGAGGAGTGTGAGAGCGGCTCC-TCACCGCTTC 464
Qy 301 agaaacacactcagacactcctcagctgtccaaatgccgaaggaatgggtcaggt 360
Db 465 AGAAACACACCTCAGACACTGCCCTCAGCTGTCTCCAAATGCCGAAAGGAATGGGTCAGGT 524
Qy 361 ggagatctcttcttgacagtggaccgggacacccgtgtgtggtgtaggaagaaccagta 420

```

```

Db 525 GGAGATCTCTTCTTGACAGTGGACCGGGACACCGGTGTGTGGCTGCGAGGAACACAGTA 584
Qy 421 ccggcattattgagtgaaacacctttccagtgcttcaattgcagcctctgctcctcaatgg 480
Db 585 CCGGCAATTATTGGAGTGAACAACTTTTCCAGTGTCTCAATTGCAGCCTTGCTCAATGG 644
Qy 481 gaccgtgacactctcctgccaggagaaacagacacccgtgtgcacctgcatgaggttt 540
Db 645 GACCGTGACCTCTTCTGCGCAGGAGAAACAGACACCGGTGTGCACCTGCGCATGCANGTT 704
Qy 541 ctttctaagagaaaacagagtggtgtctcctctgtagtaactaagaaaaagcctggagtgac 600
Db 705 CTTTCTAAGAGAAAACGAGTGTGTCTNCTGTAGTAACTGTAAGAAAAGCCTGGAATGCAC 764
Qy 601 gaa 603
Db 765 NAA 767

RESULT 9
LOCUS AU124446 859 bp mRNA EST 23-OCT-2000
DEFINITION AU124446 NT2RM4 Homo sapiens cDNA clone NT2RM4000018 5', mRNA
sequence.
ACCESSION AU124446
VERSION AU124446.1 GI:10949162
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
,Y., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source Location/Qualifiers
1..859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4000018"
/clone_lib="NT2RM4"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/notes="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
BASE COUNT 197 a 247 c 220 g 192 t 3 others
ORIGIN
Query Match 68.2%; Score 582.4; DB 107; Length 859;
Best Local Similarity 98.4%; Pred. No. 3.7e-146;
Matches 597; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
Qy 1 gagttagagggccatagctgtctggcatgggctctccaccgtgctgacctgctgctgcc 60
Db 254 GAGTGAGAGCCATAGCTGTGTGGCATGGGCTCTCCACCGCTGCTGACTGCTGCTGCC 313
Qy 61 gctggtgctcctggagctgtgtggtgggaataataccctcagggttattgactggtccc 120

```

```
|||||
Db 314 ACTGCTGCTCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTATTATGGAGTGCTCC 373
Qy 121 tcaactaggggacagggaagagatagtggtgtgtccccaaggaataatatatccacc 180
Db 374 TCACCTAGGGGACAGGAGAGAGATAGTGTGTCTCCCAAGGAATAATATCCACCC 433
Qy 181 tcaaaataattgatttctgtctaccagtgcacaaaggaacctacttgtacaatgactg 240
Db 434 TCAAAATAATTGCTATTGCTGTACCAAGTGCACAAAGGAACCTACTTGTACAATGACTG 493
Qy 241 tccagccgggacaggtacacgactgcaggagtgtaagacgctcctccacgcttc 300
Db 494 TCCAGCCCGGGGAGGATACGAGCTGCAGGGAGTGTGAGCGGCTCTCTCACCGCTTC 553
Qy 301 agaaacacacctcagacactgctcagctgctcccaaatgccgaaggaattgggtcaggt 360
Db 554 AGAAACACACCTCAGACACTGCTCAGCTGCTCCAAATGCCGAAGAAATGGGTCAAGT 613
Qy 361 ggagatctcttcttgacagtgagccgggacacggtgtgtgtgctgcaggagaacagta 420
Db 614 GGAGATCTCTTCTTGACAGTGGACGGGACACCCGTTGTGTGGCTGCAGGAAGAACAGTA 673
Qy 421 ccggcatatggaatgaaacctttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 674 CCGGCATTATTGGAGTGAAACCTTTTCCAGTGTCTCAATTGCAGCCTTGCTCAATGG 733
Qy 481 gaccctgacacctctctccaggagaaacagacacacggtgtgcacctgcatgcaggttt 540
Db 734 GACCTGTGACCT-TTCTGCCAGAGAAACAGAACACCGTGTGCACCTGTCATGCAGGGTT 792
Qy 541 ctttctaagaaaacagtggtgtctctgttagtaactgtagaagaaagcctgagtgac 600
Db 793 CTTTCTAAGAGAAAACGAATGTGTCTCTGNANTAACTGNAAAGAAAGCCTGGAATGCAC 852
Qy 601 gaagttg 607
Db 853 CAAGTTG 859

RESULT 10
BE876920 971 bp mRNA EST 20-OCT-2000
LOCUS 601488490F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890663 5',
DEFINITION mRNA sequence.
ACCESSION BE876920
VERSION BE876920.1 GI:10325683
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/PTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9674 row: d column: 24
High quality sequence stop: 722.
Location/Qualifiers
1. .971
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3890663"
/clone_lib="NIH_MGC_69"
```

```
/tissue_type="large cell carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
BASE COUNT 231 a 257 c 277 g 205 t 1 others
ORIGIN

Query Match 66.1%; Score 564.4; DB 141; Length 971;
Best Local Similarity 97.4%; Pred. No. 2.7e-141;
Matches 627; Conservative 0; Mismatches 11; Indels 6; Gaps 5;

Qy 1 gactgagagcccatagctgtctgcatggcctccaccgtgctgacctgctgctgccc 60
Db 128 GAGTGAAGGCCATAGCTGTCTGCATGGGCTCTCCACCGTGCCTGACCTGCTGCTCC 187
Qy 61 gctggtgctcctggagctgtgtgggaataataaccctcaggggttattggactggctcc 120
Db 188 ACTGGTCTCTCTGGAGCTGTGGTGGGAATATACCCCTCAGGGGTATTGGACTGGTCCC 247
Qy 121 tcaacctaggggacagagagagagatagtggtgtgtcccaaggaataatatccacc 180
Db 248 TCACCTAGGGGACAGGAGAGAGATAGTGTGTGTCTCCCAAGGAATAATATCCACCC 307
Qy 181 tcaaaataattcatttctgtaccagtgcacaaaggaacctacttgtacaatgactg 240
Db 308 TCAAAATAATTGCTATTGCTGTACCAAGTGCACAAAGGAACCTACTTGTACAATGACTG 367
Qy 241 tccagccgggggacagatacggactgcaggagtgtagagcgctcctcctccaccttc 300
Db 368 TCCAGGCCCGGGGACAGGATACGGACTGCAGGAGTGTGAGAGCGCTCTCTCACCGCTTC 427
Qy 301 agaaacacacctcagacactgctcagctcctcaaatgccgaagaaatgggtcaggt 360
Db 428 AGAAACACCACTCAGACACTGCCTCAGCTCTCCAAATGCCGAAGAAATGGGTCAAGT 487
Qy 361 ggagatctctcttcacagtgcacgggacacggtgtgtgtgctgcaggagaaccagta 420
Db 488 GGAGATCTCTTCTTGACAGTGGACCGGACACCGTGTGTGGCTGCAGGAAGAACACGTA 547
Qy 421 ccggcattattgagtgaaaaaccttttccagtgcttcaattgcagcctctgcctcaatgg 480
Db 548 CCGGCATTATTGAGTGAAAAACCTTTTCCAGTGTCTCAATTGCAGCCTCTG-CTCAATGG 606
Qy 481 gacctgacctctctctgccaggagaacacacgctgtgcaacctgccaatgaggttt 540
Db 607 GACCGTGCACCTCTCTCTGCCAGGAGAAACAGAACACCGCTGTGCCAATGCTCCATGCGGTTG 666
Qy 541 ctttctaagag-aaaacgagtgtct-cctgtagtaactgtaagaaaagcctgagtg 598
Db 667 CTTTCTAAGAGAAAAACGAGTGTGTCTCCCTGTAGTAACTGTAAAGAA--GCTGGAGTGC 724
Qy 599 acgaagtgtgctaccgccagattgagaattgaaagggcactga 642
Db 725 CGAAGTTGTG-CTAACCCAGATTGAGATGTTTAGGCCCGAGA 767

RESULT 11
AUI37990 772 bp mRNA EST 25-OCT-2000
LOCUS AUI37990 PLACE1 Homo sapiens cDNA clone PLACE1007638 5', mRNA
DEFINITION sequence.
ACCESSION AUI37990
VERSION AUI37990.1 GI:10999511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 772)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
```


Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
 HRI human cDNA project
 Unpublished (2000)
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3951
 Fax: 81-438-52-3952
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

TITLE
JOURNAL
COMMENT

FEATURES
 source
 1. .772
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="PLACE1007638"
 /clone_lib="PLACE1"
 /tissue_type="placenta"
 /note="Vector: pME18SFL3"

BASE COUNT 184 a 211 c 210 g 163 t 4 others
ORIGIN

Query Match 66.0%; Score 564; DB 108; Length 772;
 Best Local Similarity 98.3%; Pred. No. 3.3e-141;
 Matches 578; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 gagtggagggccatagctgtctggcatgggctctccaccgtgcctgacctgctgctgcc 60
 |||||
 Db 166 GAGTGAGAGGCCATAGCTGTCTGCGATGGGCTCTCCACCGTGCCTGACCTGCTGCC 225
 QY 61 gctggtctcctggagctgtgttggtggaatataccctcaggggttattggaactggtccc 120
 |||||
 Db 226 ACTGTGCTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGTGACTGGTCCC 285
 QY 121 tcacctaggagcaggagagagatagtggtgtgtccccaaggaaatataccacc 180
 |||||
 Db 286 TCACCTAGGGCAGGAGAGAGATAGTGTGTGTCTCCCAAGAAATATATCCACCC 345
 QY 181 tcaaaataattcgtattgtgtacaaagtgcacaaaggaaacctacttgtacaatgactg 240
 |||||
 Db 346 TCAAAATAATTGATTTGCTGTACCAAGTGCACAAAGGAACCTACTGTACATGACTG 405
 QY 241 tcaggcccggggcaggatagcaggactcaggagtggtgagagcggtctctcaccgttc 300
 |||||
 Db 406 TCCAGGCCCGGGCAGGATACGGACTGCAGGAGTGTGAGAGCGGNTCTTCACCGCTTC 465
 QY 301 agaaaaccactcagacactgcctcagctgtccaaatgcgaaaggaaatgggtcaggt 360
 |||||
 Db 466 AGAAACCACTTCAGACACTGCCCTCAGCTGCTCCAAATGCCGAAAGGAATGGTCAAGT 525
 QY 361 ggagatctctcttgcacagtgaggccgggacacagctgtgtgctgcaggaagaaccagta 420
 |||||
 Db 526 GGAGATCTTCTTGACAGTGGACCGGGACACCGTGTGTCGTCGAGAGAACACAGTA 585
 QY 421 ccggcattattggagtgaaacacctttccagtgcttcaattgcagcctctcctcctcaatgg 480
 |||||
 Db 586 CCGGCATTATTGGAGTGAAACCTTTTCCAGTGTCTCAATTGCAGCCTCTGCCCTCAATGG 645
 QY 481 gaccgtgacactcctctgcaggagaaacagaaacacagctgtgcacctgcaggttt 540
 |||||
 Db 646 GACCGTCAACTCTCCCTGCCAGGAGAAACAGAACACCGTGTGCACCTGCCATGCAAGTTT 705
 QY 541 ctctctaa-gagaaaacagtggtgtctctctgtagttaactgtgaagaaa 587
 |||||
 Db 706 CTTTCTAAGGAGAAACGANTGTCTCTCTGTTGTTACTGTGTANGAA 753

RESULT 12

AUI25680
LOCUS
DEFINITION
 AUI25680 NT2RM4 Homo sapiens cDNA clone NT2RM4002005 5', mRNA sequence.
ACCESSION
 AUI25680
VERSION
 AUI25680.1 GI:10950396
KEYWORDS
 EST.
SOURCE
 human.
ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
 1 (bases 1 to 817)
 Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and Isogai,T.
TITLE
 HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3951
 Fax: 81-438-52-3952
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES
 source
 1. .817
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="NT2RM4002005"
 /clone_lib="NT2RM4"
 /cell_type="teratocarcinoma"
 /cell_line="NT2"
 /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"

BASE COUNT 182 a 238 c 211 g 182 t 4 others
ORIGIN

Query Match 64.4%; Score 550.2; DB 107; Length 817;
 Best Local Similarity 97.9%; Pred. No. 1.7e-137;
 Matches 555; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 gagtggagggccatagctgtctggcatgggctctccaccgtgcctgacctgctgctgcc 60
 |||||
 Db 249 GAGTGAGAGGCCATAGCTGTCTGCGATGGGCTCTCCACCGTGCCTGACCTGCTGCC 308
 QY 61 gctggtctcctggagctgtgttggtgggaatataccctcaggggttattggactggtccc 120
 |||||
 Db 309 ACTGTGCTCTCTGGAGCTGTGTGGGAATATACCCCTCAGGGGTATTGTGACTGGTCCC 368
 QY 121 tcacctaggagcaggagagagatagtggtgtgtccccaaggaaatataccacc 180
 |||||
 Db 369 TCACCTAGGGGACAGGGAGAGAGATAGTGTGTGTCTCCCAAGAAATATATCCACCC 428
 QY 181 tcaaaataattcgtattgtgtgtaccgaagtgcacaaaggaaacctacttgcacaaatgactg 240
 |||||
 Db 429 TCAAAATAATTGATTTGCTGTACCAAGTGCACAAAGGAACCTACTTGTACAAATGACTG 488
 QY 241 tcaggcccggggcaggatagcaggactcaggagtggtgagagcggtctctcaccgttc 300
 |||||
 Db 489 TCCAGGCCCGGGCAGGATACGGACTGCAGGAGTGTGAGAGCGGCTCTTCCACCTTC 548
 QY 301 agaaaaccactcagacactgcctcagctgtccaaatgcgaaaggaaatgggtcaggt 360
 |||||
 Db 549 AGAAACCACTTCAGACACTGCCTCAGCTGTCTCCAAATGCCGAAAGGAATGGGTCAAGT 608
 QY 361 ggagatctctcttgcacagtgaggccgggacaccggtgtgtggtgctgcaggaagaaccagta 420


```

Db 609 GGAGATCTCTTGGACAGTGGACGGGACACCGGTGTGGCTGCAGGAAGAACAGTA 668
Qy 421 ccggcattattgagtgaaaaacttttccagtgcttcaattgcagcctctgctcctaagg 480
Db 669 CCGGATATTATGGAGTGAACACTTTTNCAGTGTCTCAATTCGACGCTCTGGCTCAATGG 728
Qy 481 gaccgtcacctctcctgcccaggagaaacagacacccgtgtgcacctgcatgcaaggttt 540
Db 729 GACCGTGCACCTTTTCTGCGCAGGAGAACAGAACACCGGTGTGCACCTGCCATGCAGGNTT 788
Qy 541 ctttctaagagaaaacgagtgctc 567
Db 789 CTTTCTAAGAGAAAACGATNGGCTTC 815

RESULT 13
AUI24156
LOCUS AUI24156 706 bp mRNA EST 23-OCT-2000
DEFINITION AUI24156 NT2RM2 Homo sapiens cDNA clone NT2RM2001757 5', mRNA
sequence.
ACCESSION AUI24156
VERSION AUI24156.1 GI:10948872
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 706)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
,Y., Sugano,S., Isogai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1..706
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM2001757"
/cell_type="teratocarcinoma"
/cell_lines="NT2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
BASE COUNT 175 a 192 c 185 g 150 t 4 others
ORIGIN

Query Match 62.0%; Score 529.8; DB 107; Length 706;
Best Local Similarity 97.2%; Pred. No. 5.3e-132;
Matches 559; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

Qy 1 gagttagagccatagctgtctggcatggccctctccacgtgcctgacctgctgcc 60
Db 126 GAGTAGAGGCCATAGCTGTCTGGCATGGCCCTCTCCACCGTGCCTGACCTGCTGCC 185
Qy 61 gctggtgctcctggagctgttgggtgggaataaccctcaggggttattggactgtccc 120
Db 186 ACTGGTCTCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTATTGGACTGTC 245

```

```

Qy 121 tcacctaggggacagggagagagagatagtgtgtgtcccccaaggaaaaatatccacc 180
Db 246 TCACCTAGGGGACAGGGAGAGAGAGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 305
Qy 181 tcaataataattcattgtctgtaccagtgccacaaaggaaacctactgttacaatgactg 240
Db 306 TCAAAATAAATTCGATTGTCTGTCAAGTGCACAAAGGAACCTTACTTGTACAATGACTG 365
Qy 241 tcaggcccccgggcaggatcacgagctcagggagtgagagcggctccttcacgcgttc 300
Db 366 TCCAGGCCCGGGCAGGATACGGACTCGAGGAGTGTGAGAGCGGCTCTCTCACCGCTTC 425
Qy 301 agaaaaccacctcagacactgcctcagctcctcaaatgccgaagaaaatgggtcaggt 360
Db 426 AGAAAACCACTCAGACACTGCCTCAGCTGTCTCCAAATGCCGAAAGAAATGGGTCAAGT 485
Qy 361 ggagatctcttcttgacagtggaccgggacacccgtgtgtgtgtgcagggaagaccagta 420
Db 486 GGAGATCTCTTCTTGCACAGTGGACCGGGACACCGCTGTGTGTGTGTGTGTGTGTGTGT 545
Qy 421 ccggcattattgagtgaaaaacttttccagtgcttcaattgcagcctctcctcaatgg 480
Db 546 CCGGCATTATTGGAGTGAAAACCTTTTCCAGTGTCTCAATTCGAGCCTCTGCCCTCAATGG 605
Qy 481 ga-ccgtgcacctctcctgccaggagagaaacagacacccgtgtgcacctgacctcaggt 539
Db 606 GACCGGTGCACCTCTCTCTGCGCAGGAGAAACAG-ACACCGTGTGCACCTGCCATGCAGGT 664
Qy 540 tcttctaagagaaaacgagtgctgtctcctctagt 574
Db 665 TCTTTCTAAGAGAAACCAACCTNGCTCCTCTGTATACT 699

RESULT 14
AUI42163
LOCUS AUI42163 802 bp mRNA EST 25-OCT-2000
DEFINITION AUI42163 THYRO1 Homo sapiens cDNA clone THYRO1001877 5', mRNA
sequence.
ACCESSION AUI42163
VERSION AUI42163.1 GI:11003684
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 802)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1..802
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="THYRO1001877"
/cell_type="thyroid gland"
/note="Vector: pME18SFL3"
BASE COUNT 179 a 231 c 212 g 177 t 3 others
ORIGIN

```

[illegible]

Search completed: August 14, 2001, 05:58:16
Job time: 1293 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2001, 05:35:08 ; Search time 20.59 Seconds
(without alignments)
1407.227 Million cell updates/sec

Title: US-09-599-400A-9

Perfect score: 1231

Sequence: 1 MGLSTVPDLLPLVLELLV.....ENVKGTEDSGTTLPLVRP 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	873	70.9	189	6	Q97530 canis famil
2	866	70.3	189	6	Q95185 felis silve
3	213	17.3	380	4	Q00280 homo sapien
4	208	16.9	253	4	Q00276 homo sapien
5	208	16.9	418	4	Q00275 homo sapien
6	205.5	16.7	277	4	O14866 homo sapien
7	205.5	16.7	426	4	O14865 homo sapien
8	204	16.6	417	11	Q920W1 mus musculu
9	203.5	16.5	175	4	Q9UME5 homo sapien
10	203.5	16.5	178	4	Q9UME0 homo sapien
11	203.5	16.5	181	4	Q9UME1 homo sapien
12	200.5	16.3	147	11	Q9ER63 mus musculu
13	199.5	16.2	357	13	Q9DF34 brachydanio
14	199	16.1	387	13	Q9PVD4 xenopus lae
15	198.5	16.1	141	11	Q9ER62 mus musculu
16	188	15.3	302	13	Q9PUS0 salvelinus
17	182.5	14.8	285	13	Q9DGH7 gallus gall
18	179	14.5	320	14	O57079 cowpox viru
19	179	14.5	322	14	O72761 cowpox viru

20	176	14.3	459	11	Q62327 mus musculu
21	175.5	14.3	312	13	Q9DGH8 gallus gall
22	174.5	14.2	320	14	O57091 ectromelia
23	174.5	14.2	320	14	O57300 ectromelia
24	174.5	14.2	347	14	O57119 cowpox viru
25	174	14.1	347	14	O57115 cowpox viru
26	174	14.1	350	14	O57123 cowpox viru
27	174	14.1	351	14	O57121 cowpox viru
28	173.5	14.1	438	13	Q9DFV0 brachydanio
29	172.5	14.0	349	14	O57100 monkeypox v
30	172.5	14.0	360	14	O57118 cowpox viru
31	171.5	13.9	316	14	O57092 ectromelia
32	171.5	13.9	348	14	O57277 monkeypox v
33	171.5	13.9	482	11	O88734 mus musculu
34	171	13.9	349	14	O57305 cowpox viru
35	171	13.9	355	14	O85308 cowpox viru
36	169.5	13.8	348	14	O57103 monkeypox v
37	169.5	13.8	348	14	O57108 monkeypox v
38	169	13.7	326	14	O57120 cowpox viru
39	169	13.7	351	14	O73559 cowpox viru
40	168	13.6	372	4	Q9UHP4 homo sapien
41	168	13.6	401	4	O00300 homo sapien
42	167.5	13.6	349	14	O57291 monkeypox v
43	167.5	13.6	349	14	O57099 monkeypox v
44	167.5	13.6	349	14	O57101 monkeypox v
45	167.5	13.6	349	14	O57102 monkeypox v

ALIGNMENTS

RESULT 1

O97530 ID O97530 PRELIMINARY; PRT: 189 AA.
AC O97530;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Duthie S., Nasir L., Argyle D.J., Eckersall P.D.;
RT "Canine tumor necrosis factor receptor, partial cds.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF013955; AAD01516.1; -
DR HSSP; P19438; 1TNR.
DR InterPro; IPR000561; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR SMART; SM00208; TNFR; 1.
DR Receptor.
FT NON_TER 189 189
SQ SEQUENCE 189 AA; 21324 MW; 5D3AD6A5676BFE99 CRC64;

Query Match 70.9%; Score 873; DB 6; Length 189;

Best Local Similarity 81.9%; Pred. No. 2.5e-83;

Matches 154; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MGLSTVPDLLPLVLELLVGVSGVGLVPHLGDREKRDSCVQGGKYIHQNNISICT 60

Db 1 MGLPTVPGLLPLVLLALLEIYPSVTALVPHPRNRKRAILCPQGGKYIHPQDDSICT 60

Qy 61 KCHKGTLYLNDGPGQDTCDECEGSGTASENHLRHCLSCSKCKEMGQVEISSCTVD 120

```
Db 61 KCHKTYLYNDGPGGLDTCRECEGTFTASENHLRQCLSCSKCKEMNQVEISPCTVY 120
Qy 121 RTVCGCRKNQYRHHWSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
Db 121 RTVCGCRKNQYRHHWSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
Qy 181 SCSNCKKS 188
Db 181 SCVNCKKN 188

RESULT 2
Q95185 PRELIMINARY; PRT; 189 AA.
AC Q95185;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).
GN TNFR-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID-9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Duthie S., Nasir L., Eckersall P.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; -.
DR Pfam; PF00020; TNFR_C6; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR SMART; SM00208; TNFR; 1.
FT NON_TER 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 70.3%; Score 866; DB 6; Length 189;
Best Local Similarity 82.4%; Pred. No. 1.3e-82;
Matches 155; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MGLSTVPDLLPLVLELLAVGYPSCVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
Db 1 MGLPTVPGLLQLPLVLLALLVEIYPLVGLVPHLRDRRAIYCPQGYIHPQNNISICT 60

Qy 61 KCHKTYLYNDGPGGLDTCRECEGTFTASENHLRQCLSCSKCKEMNQVEISPCTVD 120
Db 61 KCHKTYLYNDGPGGLDTCRECEGTFTASENHLRQCLSCSKCKEMNQVEISPCTVY 120

Qy 121 RTVCGCRKNQYRHHWSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
Db 121 RTVCGCRKNQYRHHWSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180

Qy 181 SCSNCKKS 188
Db 181 SCVNCKKN 188

RESULT 3
ID Q00280 PRELIMINARY; PRT; 380 AA.
AC Q00280;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Db 61 KCHKTYLYNDGPGGLDTCRECEGTFTASENHLRQCLSCSKCKEMNQVEISPCTVY 120
Qy 121 RTVCGCRKNQYRHHWSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180
Db 121 RTVCGCRKNQYRHHWSENLFQCFNCSCLNGTVHLSQCKQNTVCTCHAGFFLRNECV 180

Qy 181 SCSNCKKS 188
Db 181 SCVNCKKN 188

RESULT 4
ID Q00276 PRELIMINARY; PRT; 253 AA.
AC Q00276;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Screation G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94503; AAC51308.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; -.
DR Pfam; PF00020; TNFR_C6; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.

Db 181 TSTLGSCPE--RCAAVC-GWRQNEAGMEALTPPPATHLSPLDSAHILLAP 227
Qy 183 ----SNCKKSLCTKLCPLPOIENVKTE-----DSGTTVLLP 215
Db 181 TSTLGSCPE--RCAAVC-GWRQNEAGMEALTPPPATHLSPLDSAHILLAP 227

Query Match 17.3%; Score 213; DB 4; Length 380;
Best Local Similarity 28.3%; Pred. No. 3e-14;
Matches 65; Conservative 24; Mismatches 95; Indels 46; Gaps 11;

Qy 15 LLELLGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICTCKHKGTYLYNDGPG 74
Db 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

Qy 75 PGQDTDCRECEGSFTASENHLR-HCLSCSKCKEMQVEISSCTVDRTVCGCRKNQYR 133
Db 75 PGQDTDCRECEGSFTASENHLR-HCLSCSKCKEMQVEISSCTVDRTVCGCRKNQYR 133

Qy 64 PCGNSTCLVCPQDTFLAWENHNSECARCOACDEQAQVALENCASVADTCGCKPGWV 123
Db 64 PCGNSTCLVCPQDTFLAWENHNSECARCOACDEQAQVALENCASVADTCGCKPGWV 123

Qy 134 HYWSENLFQ-----FNCISCLN-GTVH-----LSCQKQNTVCTCHAGFFLRNECVSC- 182
Db 124 EC---QVSSQCVSSSPFYCQPCDLCGALHRRHTRLCRRDTCGCTCLPGFVEHGDGCVSCP 180

Qy 183 ----SNCKKSLCTKLCPLPOIENVKTE-----DSGTTVLLP 215
Db 181 TSTLGSCPE--RCAAVC-GWRQNEAGMEALTPPPATHLSPLDSAHILLAP 227
```

```
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Screation G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94510; AAC51315.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000488; -.
DR InterPro; IPR000561; -.
DR Pfam; PF00020; TNFR_C6; 2.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR SMART; SM00005; DEATH; 1.
SQ SEQUENCE 380 AA; 41192 MW; ED19B586ADD947B7 CRC64;

Query Match 17.3%; Score 213; DB 4; Length 380;
Best Local Similarity 28.3%; Pred. No. 3e-14;
Matches 65; Conservative 24; Mismatches 95; Indels 46; Gaps 11;

Qy 15 LLELLGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICTCKHKGTYLYNDGPG 74
Db 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

Qy 75 PGQDTDCRECEGSFTASENHLR-HCLSCSKCKEMQVEISSCTVDRTVCGCRKNQYR 133
Db 75 PGQDTDCRECEGSFTASENHLR-HCLSCSKCKEMQVEISSCTVDRTVCGCRKNQYR 133

Qy 64 PCGNSTCLVCPQDTFLAWENHNSECARCOACDEQAQVALENCASVADTCGCKPGWV 123
Db 64 PCGNSTCLVCPQDTFLAWENHNSECARCOACDEQAQVALENCASVADTCGCKPGWV 123

Qy 134 HYWSENLFQ-----FNCISCLN-GTVH-----LSCQKQNTVCTCHAGFFLRNECVSC- 182
Db 124 EC---QVSSQCVSSSPFYCQPCDLCGALHRRHTRLCRRDTCGCTCLPGFVEHGDGCVSCP 180

Qy 183 ----SNCKKSLCTKLCPLPOIENVKTE-----DSGTTVLLP 215
Db 181 TSTLGSCPE--RCAAVC-GWRQNEAGMEALTPPPATHLSPLDSAHILLAP 227

RESULT 4
ID Q00276 PRELIMINARY; PRT; 253 AA.
AC Q00276;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Screation G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94503; AAC51308.1; -.
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000561; -.
DR Pfam; PF00020; TNFR_C6; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
```

```

DR SWART; SM00208; TNFR; 1.
SQ SEQUENCE 253 AA; 26934 MW; 4CD06775B68E9292 CRC64; 9;

Query Match 16.9%; Score 208; DB 4; Length 253;
Best Local Similarity 28.9%; Pred. No. 6.7e-14;
Matches 57; Conservative 22; Mismatches 86; Indels 32; Gaps

QY 15 LLELLVGYPGVI GLVPHLGDREKRDVCPQGKYIHPQNNISICCTKCHKGTLYLNDPCG 74
   ||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

QY 75 PGQDTRCECEGSGFTASENHLR-HCLSCSKCREMGQVEISSCTVDTRDTVCGCRKNOYR 133
   |:::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 PCGNSTCLVCPQDFTLAWENHNNSECARCQACDEQASQVALENSAVADTRCGCKPGWVF 123

QY 134 HYWSENLFQC-----FNCISCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC- 182
   ||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 124 EC---QVSSQCVSSPFFVCPCLDCGALHRTRLLCSRRDTCGTCGTCLPFGYEHGDCVSCP 180

QY 183 ----SNCKKSLECTKLC 195
   ||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 TSTLGSQPE--RCAAVC 195

RESULT 5
O00275 PRELIMINARY; PRT; 418 AA.
AC O00275;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RS SEQUENCE FROM N.A.
RA MEDLINE=9727273; PubMed=9114039;
RA Sreaton G.R., Xu X.N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "Largd: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR EMBL; U94502; AAC51307.1; -
DR HSSP; P19438; 1EXT.
DR InterPro; IPR000488; -
DR InterPro; IPR000561; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 2.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR SMART; SM00005; DEATH; 1.
SQ SEQUENCE 418 AA; 45456 MW; 54B48F8B35C620E2 CRC64;

Query Match 16.9%; Score 208; DB 4; Length 418;
Best Local Similarity 28.9%; Pred. No. 1.1e-13;
Matches 57; Conservative 22; Mismatches 86; Indels 32; Gaps

QY 15 LLELLVGYPGVI GLVPHLGDREKRDVCPQGKYIHPQNNISICCTKCHKGTLYLNDPCG 74
   ||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

QY 75 PGQDTRCECEGSGFTASENHLR-HCLSCSKCREMGQVEISSCTVDTRDTVCGCRKNOYR 133
   |:::| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 PCGNSTCLVCPQDFTLAWENHNNSECARCQACDEQASQVALENSAVADTRCGCKPGWVF 123

QY 134 HYWSENLFQC-----FNCISCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC- 182
   ||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```



```

"LRD: a new lymphoid-specific death domain containing receptor
regulated by alternative pre-mRNA splicing.";
Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
EMBL: U94505; AAC51310.1; -.
DR HSSP: P19438; 1EXT.
DR InterPro: IPR000561; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 2.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR SMART: SM00208; TNFR; 1.
KW Receptor.
SQ SEQUENCE 181 AA; 19432 MW; 59A4FEDBBB46E369 CRC64;

Query Match 16.5%; Score 203.5; DB 4; Length 181;
Best Local Similarity 30.2%; Pred. No. 1.4e-13;
Matches 54; Conservative 19; Mismatches 81; Indels 25; Gaps 7

QY 15 LLELVGYPSGVIGLVPHLGDREKRSVCPQGYIHPQNNISICCTCKHKGTYLYNDPCG 74
||:|:| | | | | | | | | | | | | | | | | | | |
Dd 15 LLLVLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63

QY 75 PQQDTDCRECSGFTASENHLR-HCLSCSKCKRMGQVEISSCTVDRTVCGCRKNQYR 133
| : : | | | | | | | | | | | | | | | | | | | |
Dd 64 PCGNSCTLVCPQDPTFLAWENHNHSECAQCACDEQASVALENESAVADTRCGCRPGWVF 123

QY 134 HWYSENIFQC-----FNCSLCLN-GTVH---LSCOEKONTVCTCHAGFFLRENECVSC 182
: : : | | | | | | | | | | | | | | | | | | | |
Dd 124 EC---QVSQCVSSPFYQPCDCLDGALHRTLLCSRRDTCGTCIPGFYEHGDCVCVSC 179

RESULT 12
QY063 PRELIMINARY; PRT; 147 AA.
AC QY063;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR P60 HOMOLOGUE 1.
GN TNFRH1.
OS Mus musculus domesticus (western European house mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10092;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20519229; Pubmed=11063728;
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
RA Lane N., Reik W., Walter J.;
RT "Sequence and functional comparison in the Beckwith-Wiedemann region;
RT Implications for a novel imprinting centre and extended imprinting.";
RL Hum. Mol. Genet. 9:2691-2706(2000).
DR EMBL; AJ278264; CAC16405.1; -.
KW Receptor.
SQ SEQUENCE 147 AA; 16253 MW; 7644271340517DC9 CRC64;

Query Match 16.3%; Score 200.5; DB 11; Length 147;
Best Local Similarity 33.6%; Pred. No. 2.4e-13;
Matches 42; Conservative 16; Mismatches 60; Indels 7; Gaps 4;

QY 44 CPQGYIHPQNNISICCTCKHKGTYLYNDPCPGQDTCRECSGFTASENHLRHLCS 103
| : | : | : | | | | | | | | | | | | | | | | | | | |
Dd 9 CPDGEY---QNSNDVCCCTPCSGTVPKAPCK1PTHQGCQCKPHGT7TKDNLGLHDCELCS 65

QY 104 KCRKMGQVEISSCTVDRTVCGCRKNQYRHWYSENIFQCFNCSLCLNG-TVHLSQCEKQ 162
| : | : | : | | | | | | | | | | | | | | | | | | | |
Dd 66 TCDKQNMV--ADGSATSDRCEQIGLY-YDPKFPESCRPTCKPGIPVQECNSTA 122

QY 163 NTVCT 167
|||||

```


Db 123 NTVCs 127

RESULT 13

Q9DF34

ID Q9DF34 PRELIMINARY; PRT; 357 AA.

AC Q9DF34;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE DEATH RECEPTOR.

OS Brachydanio rerio (Zebrafish) (Zebra danio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Rasbora; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RA Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;

RT "Stimulation of erythropoiesis by inhibiting a new hematopoietic death

RT receptor in transgenic zebrafish.";

RL Nat. Cell Biol. 0:0-0(2000).

DR EMBL; AF302789; AAC21396.1; .

KW Receptor.

SQ SEQUENCE 357 AA; 40662 MW; 1652B4840D9EEDBA CRC64;

Query Match 16.28; Score 199.5; DB 13; Length 357;

Best Local Similarity 27.68; Pred. No. 7.2e-13;

Matches 60; Conservative 27; Mismatches 79; Indels 51; Gaps 9;

QY 10 LLPVLVLELLVGIYPGSGVIGLVPH-LGDREKRDVCPQG-KYIHPQNNISICTKCHKGT 67

DB 6 LLVLLLVNVAARSHGDLAWHRSVKNRLSRDVSRCREGLYPH---ENICCLNCPAGTY 62

QY 68 LYNDPCPGPGQDTCRECEGSGSFTASENHLRCLSCSKCKEMGQVEISSCTVDRDVTGCG 127

DB 63 VKKACAAAAGKGVACPEFDYTEHDHLLKICISCDKCR--IDQETIEKCTSTQNTCKC 120

QY 128 RKNQYRHWSENLFQCNCNCLGTVHLSQEQKQNTVCTCHAGFFLRNECVSGSNCKK 187

DB 121 R-----NGSFCL-----PDQAC-----EYCKKCSRCKE 143

QY 188 SLECTKLC-----LPOIENVKGTEDSCT-TVLLPLV 217

DB 144 DEETKESCTAISNVCKRNSPGSSTWTFIVIMPLI 180

RESULT 14

Q9PVD4

ID Q9PVD4 PRELIMINARY; PRT; 387 AA.

AC Q9PVD4;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE P75-LIKE TRANSMEMBRANE PROTEIN FULLBACK.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RA Hick E., Sun B.I., Collins-Racie L., Lavallie E., Sive H.L.;

RT "Identification and Characterization of fullback, a Novel Posteriorly-

RT Expressed Xenopus Gene.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF131890; AAD54072.1; .

DR HSP; P07174; INGR.

DR InterPro; IPR000488; .

DR InterPro; IPR001368; .

DR Pfam; PF00020; TNFR_c6; 4.

DR Pfam; PF00531; death; 1.

Search completed: August 14, 2001, 05:38:06
Job time: 178 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2001, 05:28:03 ; Search time 18.64 Seconds

(without alignments)
712.267 Million cell updates/sec

Title: US-09-599-400A-9
Perfect score: 1231
Sequence: 1 MGLSTVPDLLPLVLELLV.....ENVKGTDSGTTVLLPLVRP 219

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_0601.*
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1219	99.0	280	22	Tnfr1 protein. Un
2	1219	99.0	371	11	Tumour Necrosis Fa
3	1219	99.0	455	12	30kD TNF inhibitor
4	1219	99.0	455	12	Human 55kD TNF-bin
5	1219	99.0	455	13	TNF-alpha 55kD rec
6	1219	99.0	455	14	Lambda derived TNF
7	1219	99.0	455	16	p55 TNF-R. Homo s
8	1219	99.0	455	20	Human tumour necro
9	1219	99.0	455	21	Human tumour necro
10	1219	99.0	455	21	Human TNFR 1. Hom
11	1219	99.0	455	21	Human TNFR 1. Hom

12	1219	99.0	455	21	Human tumour necro
13	1219	99.0	455	21	TNF-R1 death recep
14	1219	99.0	455	22	Human tumour necro
15	1219	99.0	455	22	Human 30 kDa TNF 1
16	1213	98.5	455	13	TNF-alpha binding
17	1210	98.3	433	14	Mutant p55 tumour
18	1210	98.3	443	14	Mutant p55 tumour
19	1210	98.3	455	14	p55 Tumour necrosi
20	1210	98.3	455	14	Mutant p55 tumour
21	1209	98.2	455	12	Type I TNF recepto
22	1208.5	98.2	909	19	Human Fas protein.
23	1203	97.7	455	11	Human Tumour Necro
24	1192	96.8	211	20	Tumour necrosis fa
25	1192	96.8	311	20	Tumour necrosis fa
26	1192	96.8	366	20	Tumour necrosis fa
27	1192	96.8	397	20	Tumour necrosis fa
28	1192	96.8	417	20	Tumour necrosis fa
29	1192	96.8	420	20	Tumour necrosis fa
30	1189	96.6	453	22	Human TNFR 1. Hom
31	1130	91.8	199	13	Truncated TNF-alpha
32	1089	88.5	309	16	TNF-R-GBPH fusion
33	1089	88.5	451	16	TNF-R-GBP 130 fusi
34	1089	88.5	547	16	TNF-R-GBPH fusion
35	1089	88.5	900	16	TNF-R-GBP 130 fusi
36	1088	88.4	1245	16	TNF-R-Pl. vivax Du
37	1088	88.4	1604	16	TNF-R-EBA 175 fusi
38	999	81.2	884	16	TNF-R-GBP 130 fusi
39	992.5	80.6	336	18	TBP(20-190)/hcg-be
40	979	79.5	285	18	TBP(20-190)/hcg-al
41	946	76.8	168	13	Truncated TNF-alpha
42	941	76.4	161	13	Native 30 kD TNF 1
43	941	76.4	161	19	Human soluble tumo
44	941	76.4	161	19	Soluble tumour nec
45	941	76.4	161	20	Tumour necrosis in

ALIGNMENTS

RESULT 1

AA866979
ID AA866979 standard; Protein; 280 AA.

XX AC AA866979;

XX DT 19-APR-2001 (first entry)

XX DE Tnfr1 protein.

XX KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
XX KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
XX KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
XX KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
XX KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
XX KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
XX KW ischaemia; Parkinson's disease.

XX OS Unidentified.

XX PN WO200103719-A2.

XX PD 18-JAN-2001.

XX PF 07-JUL-2000; 2000WO-US18667.

XX PR 09-JUL-1999; 99US-0350670.

XX PR 09-DEC-1999; 99US-0457647.

XX XX (AMGE-) AMGEN INC.

XX XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX XX WPI; 2001-103031/11.

XX Treating conditions leading to bone loss such as rheumatoid arthritis,
 PT multiple sclerosis and asthma, comprises administering an
 PT osteoprotegerin protein in conjunction with e.g. inhibitors of
 PT interleukin and tumor necrosis factor alpha
 XX Disclosure; Fig 2; 316pp; English.
 XX The present invention relates to a method for treating conditions leading
 CC to bone loss. The method comprises administering a purified and isolated
 CC osteoprotegerin (OPG) protein (AA057836-AA057838 and AA066974-AA066976)
 CC in conjunction with other substances such as tumor necrosis factor-alpha
 CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
 CC modulators, fibroblast growth factor (FGF)-1-10 modulators and/or platelet
 CC activating factor (PAF) antagonists. The method is useful for treating
 CC conditions leading to bone loss such as rheumatoid arthritis, multiple
 CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
 CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
 CC graft-versus-host disease (GVHD). Other diseases that can be treated
 CC include acute pancreatitis, Alzheimer's disease, anorexia,
 CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
 CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
 CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
 CC psoriasis and septic shock. The present sequence was used in a sequence
 CC homology comparison.
 XX
 SQ Sequence 280 AA;

Query Match 99.0%; Score 1219; DB 22; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.2e-91;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSTVPDLLLPLVLELLVIGPSVIGLVPHLGRKDSVCPGKVIHPQNNISICT 60
 DB 1 mglstvpdlllplvlellvlgpsvlgvlphlgdrkdrsvcpqgkyihpqnnsicct 60
 QY 61 KCHKGTLYNDPCPGQDTCRECEGSGFTASENHLRHCLSCSKCRKEMGOVEISSCTVD 120
 DB 61 kchkgtlyndpcpgqgdtcdrecesgsftasenhrlhclscskcrkemgoveissctvd 120
 QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEKQNTVCTCHAGFFLRENECV 180
 DB 121 rdtvcgrknqyrhywsenlfqcfncslclngtvhlscqekqntvctchagfflrenecv 180
 QY 181 SCSCNCKKSLCTKLCPLQIENVKGTEDSGTTLPLV 217
 DB 181 scsnckkslectklcplqienvkgtdsgttvllplv 217

RESULT 2
 AAR07449
 ID AAR07449 standard; protein; 371 AA.
 XX
 AC AAR07449;
 XX
 DT 29-JAN-1991 (first entry)
 XX
 DE Tumour Necrosis Factor-Binding Protein from pTNF-BP15 cDNA.
 XX
 KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;
 KW pTNF-BP15; infectious disease; parasitic disease; cachexia;
 KW autoimmune disease; shock.
 XX
 OS Homo sapiens.
 XX
 PN EP393438-A.
 XX
 PD 24-OCT-1990.
 XX
 PF 06-APR-1990; 90EP-0106624.
 XX
 PR 21-JUN-1989; 89DE-3920282.

PR 21-APR-1989; 89DE-3913101.
 XX
 PA (BOEH) BOEHRINGER INGELHEIMINT.
 XX
 PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;
 XX
 DR WPI; 1990-321987/43.
 DR N-PSDB; AAQ06282.
 XX
 PT DNA encoding TNF binding protein and TNF- receptor - used in
 PT tumour treatment and to understand mechanismsm to TNF action
 XX
 PS Disclosure; Fig 1(1-3); 5lpp; German.
 XX
 CC Clone pTNF-Bp15 was used to construct pADTNF-BP, for transfection of
 CC e.g. COS7 cells. The expressed proteins are useful
 CC prophylactically and therapeutically to control disorders which
 CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult
 CC respiratory distress syndrome etc., or side effects of treatment with
 CC TNF-alpha). They can also be used as diagnostic reagents for
 CC assaying TNF and in study of TNF-receptor interactions.
 CC See also AAQ06282-Q06285.
 XX
 SQ Sequence 371 AA;

Query Match 99.0%; Score 1219; DB 11; Length 371;
 Best Local Similarity 100.0%; Pred. No. 1.6e-91;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSTVPDLLLPLVLELLVIGPSVIGLVPHLGRKDSVCPGKVIHPQNNISICT 60
 DB 1 mglstvpdlllplvlellvlgpsvlgvlphlgdrkdrsvcpqgkyihpqnnsicct 60
 QY 61 KCHKGTLYNDPCPGQDTCRECEGSGFTASENHLRHCLSCSKCRKEMGOVEISSCTVD 120
 DB 61 kchkgtlyndpcpgqgdtcdrecesgsftasenhrlhclscskcrkemgoveissctvd 120
 QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQCEKQNTVCTCHAGFFLRENECV 180
 DB 121 rdtvcgrknqyrhywsenlfqcfncslclngtvhlscqekqntvctchagfflrenecv 180
 QY 181 SCSCNCKKSLCTKLCPLQIENVKGTEDSGTTLPLV 217
 DB 181 scsnckkslectklcplqienvkgtdsgttvllplv 217

RESULT 3
 AAR10986
 ID AAR10986 standard; Protein; 455 AA.
 XX
 AC AAR10986;
 XX
 DT 13-MAY-1991 (first entry)
 XX
 DE 30kD TNF inhibitor precursor.
 XX
 KW Tumour necrosis factor; inhibitor.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 40..41
 FT note=" cleavage gives active protein "
 XX
 PN AU9058976-A.
 XX
 PD 24-JAN-1991.
 XX
 PF 16-JUL-1990; 90AU-0058976.
 XX
 PR 07-FEB-1990; 90US-0479661.

PR 18-JUL-1989; 89US-0381080.
 PR 11-DEC-1989; 89US-0450329.

PA (SYNE-) SYNERGEN INC.

XX WPI; 1991-073847/11.

DR N-PSDB; AAQ10883.

XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha
 PT and -beta, useful as therapeutic agent.

XX Disclosure; Fig 21; 142pp; English.

XX The sequence comprises the entire 30 kD TNF inhibitor. The clone
 CC from which the sequence was deduced was isolated from a cDNA
 CC library prepd. from RNA form U937 cells treated with PMA/PHA.
 CC The whole gene can be inserted into expression vectors for prepn.
 CC of TNF inhibitor for use in the treatment of inflammatory and
 CC degenerative diseases. The active protein is claimed (Claim 8).
 CC See also AAR10984 and AAR11001.

XX Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 12; Length 455;
 Best Local Similarity 100.0%; Pred. No. 2e-91;

Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDRKDSVCPQGYIHPQNNISICT 60

Db 1 mglstvpdlllplvlellvgyipsgviglphlgdrkrdsvcpqgyihpqnnsicct 60

QY 61 KCHKGTLYLNDPCPGQDTCRECESGSFTASENHLRHLCSCKRKMGMQVEISSCTVD 120

Db 61 kchkgtlylndcpgpgqdtcrecesgsftasenhrlhrlcsckrkemgqvveissctvd 120

QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQEKQNTVCTCHAGFFLRENECV 180

Db 121 rdtvcgcrknqyrhywsenlfcfncslcngtvlhlsceqkntvtctchagfflrenecv 180

QY 181 SCSCNCKKSLLECTKLCPLQIENVKGTEDSGTTVLLPLV 217

Db 181 scsnckkslectkclcpqienvkgtdsgttvllplv 217

RESULT 4

AAAR11082

ID AAR11082 standard; Protein; 455 AA.

XX AC AAR11082;

XX 24-MAY-1991 (first entry)

XX Human 55kD TNF-binding protein.

XX Tumour Necrosis Factor; binding proteins; septic shock;
 KW autoimmune glomerulonephritis; lymphokine; cytokine.

XX Key Location/Qualifiers

FT Modified-site 54 /label= putative N-glycosylation site

FT Modified-site 145 /label= putative N-glycosylation site

FT Modified-site 151 /label= putative N-glycosylation site

FT Modified-site 270 /label= putative N-glycosylation site

FT Region 212..230 /label= putative N-glycosylation site

FT Peptide 1..28 /label= transmembrane region

XX /label= signal peptide

PN EP417563-A.

XX 20-MAR-1991.

XX 31-AUG-1990; 90EP-0116707.

XX 20-APR-1990; 90CH-0001347.

PR 12-SEP-1989; 89CH-0003119.

PR 08-MAR-1990; 90CH-0000746.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 PI Schlaeager EJ;

XX WPI; 1991-081851/12.

DR N-PSDB; AAQ10955.

XX Insoluble tumour necrosis factor binding proteins - and DNA
 PT encoding them, useful in pharmaceutical prods. and for antibody
 PT prodn.

XX Claim 1; Fig 1; 26pp; German.

XX Partial amino acid sequences were determined for the 55 and 75kD
 CC TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
 CC synthesised based on these partial sequences. The primers were used
 CC to produce a cDNA fragment for use as a probe to screen a human
 CC placental cDNA bank constructed in lambda gt11. Positive clones were
 CC identified and sequenced. DNA constructs comprising the TNF-BP coding
 CC sequence may also contain a fragment encoding a human Ig domain.
 CC Recombinant constructs are used to transform cells to confer
 CC improved TNF-binding properties.
 CC See also AAQ10956.

XX Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 12; Length 455;

Best Local Similarity 100.0%; Pred. No. 2e-91; Mismatches 0; Indels 0; Gaps 0;
 Matches 217; Conservative 0;

QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDRKDSVCPQGYIHPQNNISICT 60

Db 1 mglstvpdlllplvlellvgyipsgviglphlgdrkrdsvcpqgyihpqnnsicct 60

QY 61 KCHKGTLYLNDPCPGQDTCRECESGSFTASENHLRHLCSCKRKMGMQVEISSCTVD 120

Db 61 kchkgtlylndcpgpgqdtcrecesgsftasenhrlhrlcsckrkemgqvveissctvd 120

QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSQEKQNTVCTCHAGFFLRENECV 180

Db 121 rdtvcgcrknqyrhywsenlfcfncslcngtvlhlsceqkntvtctchagfflrenecv 180

QY 181 SCSCNCKKSLLECTKLCPLQIENVKGTEDSGTTVLLPLV 217

Db 181 scsnckkslectkclcpqienvkgtdsgttvllplv 217

RESULT 5

AAAR24000

ID AAR24000 standard; Protein; 455 AA.

XX AC AAR24000;

XX 05-NOV-1992 (first entry)

XX TNF-alpha 55kD receptor.

XX tumour necrosis factor alpha; extracellular binding domain;
 KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
 KW malaria; viral meningitis; graft versus host disease;
 KW autoimmune disease; rheumatoid arthritis.


```
XX SQ Sequence 455 AA;
Query Match 99.0%; Score 1219; DB 14; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVIGVPSGVLGPHLGRKRDSCVPGQKYIHPQNNISICT 60
DB 1 mglstvpdlllplvlellvlgypsgvlgphlgdrekrdsvcpqgkyihpqnnsict 60
QY 61 KCHKGTLYNDPCPGQDTRCECSGSFTASENHLRHLCSCKRKEMGQVEISSCTVD 120
DB 61 kchkgtlyndpcpgqgdtrcecsgsftasenhhlrhlscskrkemgqveissctvd 120
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSCEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgcrknqyrhywsenlfqcfncslclngtvtvhlscqekqntvctchagfflrenecv 180
QY 181 SCSCNCKKSLECKLCPQIENVKGTDSGTTVLLPLV 217
DB 181 scscnckkslectklcpqienvkgtdsgttvllplv 217
RESULT 7
AAR75084
ID AAR75084 standard; Protein; 455 AA.
XX AC AAR75084;
XX DT 19-JAN-1996 (first entry)
XX DE p55 TNF-R.
XX KW p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
XX KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
XX KW phorbol myristate acetate; PMA.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 41..53
FT /note= "N terminus of soluble p55 TNF-R"
FT Modified-site 54..56
FT /note= "glycosylation site"
FT Modified-site 145..147
FT /note= "glycosylation site"
FT Modified-site 161..163
FT /note= "glycosylation site"
FT Peptide 193..210
FT /note= "peptide used in creation of chimeras"
FT Region 198..210
FT /note= "spacer region"
FT Misc-difference 201
FT /note= "major C terminus for soluble p55 TNF-R"
FT Misc-difference 202
FT /note= "essential for shedding reaction"
FT Misc-difference 203
FT /note= "minor C terminus for soluble p55 TNF-R"
FT Region 212..234
FT /note= "transmembrane region"
XX AU947542-A.
XX PD 04-MAY-1995.
XX PF 11-OCT-1994; 94AU-0075742.
XX PR 12-OCT-1993; 93IL-0107268.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX
```

```
PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
XX WPI; 1995-194342/26.
XX N-PSDB; AAQ90513.
XX New protease capable of cleaving soluble tumour necrosis factor
XX (TNF) receptor - from cell-bound TNF- receptor, useful for
XX antagonising deleterious effects of TNF.
XX Disclosure; Fig 1; 40pp; English.
XX This sequence represents human p55 tumour necrosis factor (TNF-R).
XX Expression of this receptor is regulated by shedding of the
XX extracellular receptor fragment. The p55 TNF-R can be shed in response
XX to different inducing agents, e.g. phorbol myristate acetate (PMA),
XX depending on cell type. The only region of the receptor whose structure
XX affects the shedding response is the spacer region (see AAR75012) in the
XX extracellular domain. This region is located close to a site of cleavage
XX of the molecule, and links the Cys rich module to the transmembrane
XX domain. The spacer region of the encoded protein was used to create the
XX chimeras between human p55 TNF-R and murine epidermal growth factor
XX receptor (EGF-R) that are represented by AAR75007-11. This spacer region
XX was subjected to deletion mutations (AAR75013-25) and substitutions
XX (AAR75026-47). Of the spacer region, the most important residues are
XX Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
XX important of these. The shedding of the receptor is independent of the
XX side chain identity of these residues, with the exception of a limited
XX dependence on the identity of Val 173. Mutations which alter the
XX conformation of the protein adversely effect the shedding process.
XX The mutations shown in AAR75013-47 were introduced in order to create an
XX inhibitor of a protease that is capable of cleaving the soluble TNF-R
XX from the cell bound TNF-R. Fragments of these inhibitors can be seen in
XX AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
XX inhibitors can be used for enhancing TNF function.
XX SQ Sequence 455 AA;
Query Match 99.0%; Score 1219; DB 16; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVIGVPSGVLGPHLGRKRDSCVPGQKYIHPQNNISICT 60
DB 1 mglstvpdlllplvlellvlgypsgvlgphlgdrekrdsvcpqgkyihpqnnsict 60
QY 61 KCHKGTLYNDPCPGQDTRCECSGSFTASENHLRHLCSCKRKEMGQVEISSCTVD 120
DB 61 kchkgtlyndpcpgqgdtrcecsgsftasenhhlrhlscskrkemgqveissctvd 120
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCINGTVHLSCEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgcrknqyrhywsenlfqcfncslclngtvtvhlscqekqntvctchagfflrenecv 180
QY 181 SCSCNCKKSLECKLCPQIENVKGTDSGTTVLLPLV 217
DB 181 scscnckkslectklcpqienvkgtdsgttvllplv 217
RESULT 8
AAY30934
ID AAY30934 standard; Protein; 455 AA.
XX AC AAY30934;
XX DT 18-OCT-1999 (first entry)
XX DE Human tumour necrosis factor binding protein.
XX KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
XX KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
XX KW autoimmune glomerulonephritis; cerebral malaria; immune response;
XX KW antagonist; diagnosis.
XX
```

```
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT Location/Qualifiers
XX FT 1..29
XX FT /label= signal_peptide
XX FT 30..455
XX FT Modified-site
XX FT 34
XX FT /note= "hypothetical glycosylation site"
XX FT 125
XX FT /note= "hypothetical glycosylation site"
XX FT 131
XX FT /note= "hypothetical glycosylation site"
XX FT 212..230
XX FT /note= "transmembrane region"
XX FT 250
XX FT /note= "hypothetical glycosylation site"
XX PN EP939121-A2.
XX PD 01-SEP-1999.
XX PF 31-AUG-1990; 90EP-0116707.
XX PR 20-APR-1990; 90CH-0001347.
XX PR 12-SEP-1989; 89CH-0003319.
XX PR 08-MAR-1990; 90CH-0000746.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
XX PI Schlaeger E;
XX DR WPI; 1999-480840/41.
XX DR N-PSDB; AAZ09170.
XX PT New insoluble proteins, and fragments, that bind to tumor necrosis
XX PT factor, used to treat e.g. septic shock or cerebral malaria
XX PS Claim 4a; Fig 1; 25pp; German.
XX CC This invention describes novel homogeneous insoluble proteins (I),
XX CC their (in)soluble fragments (Ia) and their salts that can bind tumour
XX CC necrosis factor (TNF). The products of the invention have
XX CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (i)
XX CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
XX CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
XX CC (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
XX CC diagnostic determination of TNF in body fluids. Antibodies raised against
XX CC (I) are used for affinity purification of (I). This sequence represents
XX CC a tumour necrosis factor binding protein described in the method of
XX CC the invention.
XX SQ Sequence 455 AA;
XX Query Match 99.0%; Score 1219; DB 20; Length 455;
XX Best Local Similarity 100.0%; Pred. No. 2e-91;
XX Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLVLELLVGIYPSGVIGLVPHLGDREKRDSCVCPQKGIHPQNNISCTCT 60
DB 1 mglstvpdlllplvlllellvglypsgviglvphlgdrekrdscvcpqgkyihpqnnsict 60
QY 61 KCHKGTLYNDPCPGQDPTDCRECSGFTASENHRLHCLSCSKCKREMGQVEISSCTVD 120
DB 61 kchkgtlyndcpgpgqddtcrecsgstasenhrlhclscskckremgqveissctvd 120
QY 121 RDTVCGRKNQRYHWSNENLFCQFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgrknqryhwsenlfcqfnscslclngtvhlscqekqntvctchagfflrenecv 180
QY 181 SCSCNCKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
```

```
DB 181 scsnckkslectklclpqienvkgtedsgttvllplv 217
RESULT 9
AAB36266
ID AAB36266 standard; Protein; 455 AA.
XX AAB36266;
XX 20-FEB-2001 (first entry)
XX Human tumour necrosis factor receptor 1.
DE Human; death domain containing receptor; DR3-V1; cancer;
KW autoimmune disorder; inflammation; cardiovascular disorder; infection;
KW neurodegenerative disease; angiogenesis.
XX Homo sapiens.
XX WO200064465-A1.
XX 02-NOV-2000.
XX 21-APR-2000; 2000WO-US10741.
XX 22-APR-1999; 99US-0130488.
XX 28-MAY-1999; 99US-0136741.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX (YUGG/) YU G.
XX (NIJJ/) NI J.
XX (GENT/) GENTZ R L.
XX (DILL/) DILLON P J.
XX (DIXI/) DIXIT V M.
XX Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;
XX WPI; 2000-687263/67.
XX Treating graft-versus-host disease, cancer, immunodeficiency or an
XX autoimmune disease comprising administering an antibody to Death Domain
XX Containing Receptor proteins and a second therapeutic agent -
XX Disclosure; Fig 3; 273pp; English.
XX The present invention provides the protein and coding sequences for two
XX death domain containing receptors, designated DR3 and DR3-V1. These
XX receptors are involved in apoptosis, and the sequences given can be used
XX in the treatment of cancers, infections, cardiovascular disorders such as
XX arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms
XX and congenital heart defects, neurodegenerative diseases including
XX Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple
XX sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,
XX and to promote angiogenesis and wound healing.
XX Sequence 455 AA;
XX Query Match 99.0%; Score 1219; DB 21; Length 455;
XX Best Local Similarity 100.0%; Pred. No. 2e-91;
XX Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLVLELLVGIYPSGVIGLVPHLGDREKRDSCVCPQKGIHPQNNISCTCT 60
DB 1 mglstvpdlllplvlllellvglypsgviglvphlgdrekrdscvcpqgkyihpqnnsict 60
QY 61 KCHKGTLYNDPCPGQDPTDCRECSGFTASENHRLHCLSCSKCKREMGQVEISSCTVD 120
DB 61 kchkgtlyndcpgpgqddtcrecsgstasenhrlhclscskckremgqveissctvd 120
QY 121 RDTVCGRKNQRYHWSNENLFCQFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
```



```

Db 121 rdtvcgrknqyrhywsenlfqfncslclngtvtvhlscqekqntvctchagfflrenecev 180
QY 181 SCSCNCKSLECTKLCPLQIENVKGTEDSGTFTVLLPLV 217
Db 181 scsnckkslectkclcpqienkvgtedsgttvllplv 217
RESULT 10
AAB37800
ID AAB37800 standard; Protein: 455 AA.
XX
AC AAB37800;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human tumour necrosis factor p55 receptor.
XX
KW Human; tumour necrosis factor; TNF; TNF-alpha; TNF-beta; p55 receptor;
KW p75 receptor; antiinflammatory; haemostatic; antibacterial; sepsis;
KW immunosuppressive; immunomodulator; cardiant; cytostatic; cachexia;
KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
KW chronic myelogenous leukaemia; inflammatory bowel disease.
XX
OS Homo sapiens.
XX
PN WO200064479-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-US11700.
XX
PR 27-APR-1999; 99US-0301274.
XX
PA (ANTI-) ANTIBODY SYSTEMS INC.
XX
PI Fredeking TM, Ignatyev GM;
XX
DR WPI; 2000-679646/66.
XX
PT Novel compositions comprising tetracycline or tetracycline-like
PT compounds for the treatment and/or prevention of acute inflammatory
PT responses and diseases, e.g. septic shock and immune complex-induced
PT colitis -
XX
PS Disclosure; Page 167-169; 183pp; English.
XX
CC The present sequence is given in a specification relating to novel
CC compositions and methods containing tetracycline or tetracycline-like
CC compounds for treating and/or preventing acute inflammatory responses and
CC diseases. Such diseases include acute inflammatory conditions associated
CC with viral haemorrhagic diseases (including diseases caused by
CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
CC disorders, acute cardiovascular events, chronic myelogenous leukaemia and
CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
CC immune complex-induced colitis, cerebrospinal fluid inflammation,
CC multiple sclerosis, inflammatory responses associated with trauma,
CC systemic inflammatory response syndrome (SIRS), adult respiratory
CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
CC and Crohn's disease.
XX
SQ Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 0;

QY 1 MGLSTVPDLLPLVLELVGIVPSGVIGLVPHLGREKRDSCVPOGKYTHPQNNSICCT 60
Db 1 mglstvpdllplvllvllvlgivpsgviglvphlgdrekrdscvpqgkyhpnqnsicct 60

```

```

QY 61 KCHKGTLYLNDPCPGQDTDCRECSGSFTASENHLRHLCLSCSKCRKMGQVEISSCTVD 120
Db 61 kchkgtlylndpcpgqgtdcrecsgsftasenhlrlclscskcrkemgqvveissctvd 120
QY 121 RDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTHTVHLSQEQKONTVCTCHAGFFLRENECV 180
Db 121 rdtvcgrknqyrhywsenlfqfncslclngtvtvhlscqekqntvctchagfflrenecev 180
QY 181 SCSCNCKSLECTKLCPLQIENVKGTEDSGTFTVLLPLV 217
Db 181 scsnckkslectkclcpqienkvgtedsgttvllplv 217

```

RESULT 11

AAB26984
ID AAB26984 standard; Protein: 455 AA.

XX AC AAB26984;

XX DT 02-FEB-2001 (first entry)

XX DE Human TNFR 1.

XX KW Human; TNFR 1; tumour necrosis factor; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
KW antiarthritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinaemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
KW cardiovascular disease; neurological disease; protein coordinate data.

XX OS Homo sapiens.

XX PN WO200056862-A1.

XX PD 28-SEP-2000.

XX PF 16-MAR-2000; 2000WO-US06831.

XX PR 24-MAR-1999; 99US-0126019.

XX PR 14-MAY-1999; 99US-0134220.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Gentz RL, Yu G, Fan P;

XX DR WPI; 2000-594575/56.

XX PT Nucleic acid molecule encoding a human tumor necrosis factor receptor,
PT known as TR9, useful for treating, preventing and diagnosing severe
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
PT and cancer -

XX PS Disclosure; Fig 2; 220pp; English.

XX CC The present sequence is TNFR 1, a member of the tumour necrosis factor
CC receptor family. A novel human tumour necrosis factor receptor,
CC designated TR9, has been isolated. The TR9 receptor is also known as
CC Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or
CC agonists are useful for treating, preventing or diagnosing common
CC variable immunodeficiency, X-linked agammaglobulinaemia, severe combined
CC immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such
CC as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,
CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,
CC cardiovascular diseases and other neurological diseases.

XX SQ Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 21; Length 455;

Best Local Similarity 100.0%; Pred. No. 2e-91; Mismatches 0; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVLPHLGDREKRDSCVPOGKYIHPQNNISICT 60
DB 1 mglstvpdlllplvlellvgiypsgvlphlgdrekrdscvpgkyihpqnnsict 60

QY 61 KCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCLSCSKCKEMGQVEISSCTVD 120
DB 61 kchkgtlyndcpgpgqdtcrecesgsftasenhrlrhclscskckemgqveissctvd 120

QY 121 RDTVCGRKNQYRHYWSENLFQCFNCSLCINGTVHLSQEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgrknqyrhywsenlfqcfncslcingtvhlsqekqntvctchagfflrenecv 180

QY 181 SCSCNCKSLKCLPQIENVKGTEDSGTTVLLPLV 217
DB 181 scscnckslcklclpqienvkgtedsgttvllplv 217

RESULT 12
AAB23446
ID AAB23446 standard; Protein; 455 AA.
XX AAB23446;
AC AAB23446;
DT 12-JAN-2001 (first entry)
DE Human tumour necrosis factor receptor 1 protein.
XX TNFR1; tumour necrosis factor receptor; polymorphism; human;
KW tumour; cancer; apoptosis; bacterial infection.
XX Homo sapiens.
XX WO2000050436-A1.
XX 31-AUG-2000.
XX 23-FEB-2000; 2000WO-US04606.
XX 23-FEB-1999; 99US-0121314.
XX (GENA-) GENAISSANCE PHARM INC.
XX (NAND/) NANDABALAN K.
XX (SCHU/) SCHULZ V P.
XX (STEP/) STEPHENS J C.
XX (CHEW/) CHEW A.
XX Nandabalan K, Schulz VP, Stephens JC, Chew A;
XX WPI; 2000-543909/49.
XX N-P5DB; AAA95105.

Polynucleotides comprising polymorphic variants of a reference sequence for tumour necrosis factor receptor 1 (TNFR1), useful for studying the biological function of TNFR1 and identifying drugs targeting the protein for treating disorders -

Claim 10; Fig 5; 79pp; English.

The present invention relates to polymorphic variants of the tumour necrosis factor receptor 1 (TNFR1) gene. The present sequence is the TNFR1 protein. The sequence of the whole gene is given in AAA95102, CC AAA95103 and AAA95104. The polymorphisms were identified by amplifying and sequencing regions of the gene. Twelve polymorphic loci CC were discovered. Of these twelve polymorphisms, four can cause a CC change in the TNFR1 protein. The TNFR1 polymorphisms may be useful CC for studying the biological function of TNFR1 as well as for CC identifying drugs targeting the protein for treatment of disorders CC related to its abnormal expression or function such as tumours, CC apoptosis related disorders and bacterial infection.

SQ Sequence 455 AA;
Query Match 99.0%; Score 1219; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91; Mismatches 0; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVLPHLGDREKRDSCVPOGKYIHPQNNISICT 60
DB 1 mglstvpdlllplvlellvgiypsgvlphlgdrekrdscvpgkyihpqnnsict 60

QY 61 KCHKGTLYNDPCPGQDPTDCRECSGSFTASENHLRHCLSCSKCKEMGQVEISSCTVD 120
DB 61 kchkgtlyndcpgpgqdtcrecesgsftasenhrlrhclscskckemgqveissctvd 120

QY 121 RDTVCGRKNQYRHYWSENLFQCFNCSLCINGTVHLSQEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgrknqyrhywsenlfqcfncslcingtvhlsqekqntvctchagfflrenecv 180

QY 181 SCSCNCKSLKCLPQIENVKGTEDSGTTVLLPLV 217
DB 181 scscnckslcklclpqienvkgtedsgttvllplv 217

RESULT 13
AAB01336
ID AAB01336 standard; Protein; 455 AA.
XX AAB01336;
AC AAB01336;
DT 25-SEP-2000 (first entry)
DE TNF-R1 death receptor.
XX ULL144; death receptor; apoptosis; programmed cell death; FAS;
KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;
KW human.
XX Homo sapiens.
XX WO2000034335-A2.
XX 15-JUN-2000.
XX 03-DEC-1999; 99WO-US26035.
XX 04-DEC-1998; 98US-0205018.
XX (SCHE) SCHERING CORP.
XX Leong C, Phillips JH;
XX WPI; 2000-423383/36.
XX Purified or recombinant polypeptide for modulating apoptosis comprises a sequence which binds to an antibody specific for ULL144 or its fragments
XX Disclosure; Page 65-67; 76pp; English.
XX A pure or recombinant polypeptide which binds to a polyclonal antibody specific for the mature ULL144 is useful for screening molecules which block induction of apoptosis or interfere with antiapoptotic activity. The polypeptide is also useful for modulating apoptosis and useful in treatment of conditions associated with abnormal physiology or development, such as cancer or degenerative conditions and for regulation of viral infection and replication. At least five different death receptors are known, which include the CD95 (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated protein (TRAMP), death receptor-6 (DR-6), and TNF-related apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.

Query Match 99.0%; Score 1219; DB 21; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGLVPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
DB 1 mglstvpdllplvlellvglvpsgviglvphlgdrekrdsvcpqgyihpqnusict 60

QY 61 KCHKGTYLYNDCPGPGQDTCRECSGSFTASENHLRHLCSCKRKMGOVEISSCTVD 120
DB 61 kchkgtylyndcpgpgqdtcrecsgsftasenhrlhclscskrkemgoveissctvd 120

QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqekqntvctchagfflrenecv 180

QY 181 SCNCKKSLECTKLCPLQIENVKGTEGTVLLPLV 217
DB 181 scnckkslectklcplqienvkgtedsgttvllplv 217

RESULT 14
AAB36697
ID AAB36697 standard; Protein; 455 AA.
AC AAB36697;
XX
PN WO200071150-A1.
XX
PD 30-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-US13515.
XX
XX 20-MAY-1999; 99US-0135164.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Wei Y, Ruben SM, Gentz RL, Ni J;
XX
DR WPI; 2001-041051/05.
XX
XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection -
XX
PS Disclosure; Fig 2; 285pp; English.
XX
XX The present invention describes the human TRID protein (tumor necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumor necrosis factor
CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
CC neutropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities, and can be used in gene therapy. The TRID polynucleotides
CC are useful for detecting complementary polynucleotides. TRID proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to

CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TRID by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TRID
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer;
CC (b) autoimmune disorders; (c) diseases associated with increased
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC present sequence represents a tumour necrosis factor receptor used in
CC comparison with TRID in the exemplification of the present invention.
XX
SQ Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 22; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGLVPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
DB 1 mglstvpdllplvlellvglvpsgviglvphlgdrekrdsvcpqgyihpqnusict 60

QY 61 KCHKGTYLYNDCPGPGQDTCRECSGSFTASENHLRHLCSCKRKMGOVEISSCTVD 120
DB 61 kchkgtylyndcpgpgqdtcrecsgsftasenhrlhclscskrkemgoveissctvd 120

QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
DB 121 rdtvcgcrknqyrhywsenlfqcfncslclngtvhlscqekqntvctchagfflrenecv 180

QY 181 SCNCKKSLECTKLCPLQIENVKGTEGTVLLPLV 217
DB 181 scnckkslectklcplqienvkgtedsgttvllplv 217

RESULT 15
AAB37677
ID AAB37677 standard; protein; 455 AA.
XX
AC AAB37677;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human 30 kDa TNF inhibitor precursor.
XX
KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human.
XX
OS Homo sapiens.
XX
PN US6143866-A.
XX
PD 07-NOV-2000.
XX
XX 19-JAN-1995; 95US-0375242.
XX
XX 19-JUL-1990; 90US-0555274.
PR 09-JUL-1993; 93US-0090366.
PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
XX (AMGE-) AMGEN INC.
PA Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
XX Vanderslice RW, Vannice J, Kohno T;
PI
XX WPI; 2001-006443/01.
DR N-PSDB; AAC83946.
XX

PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
TNF -
XX
XX
PS Example 6; Fig 21; 82pp; English.
XX
CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC novel TNF inhibitors of the present invention are useful as therapeutic
CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC for treating inflammatory and degenerative diseases mediated by TNF. The
CC present sequence is the precursor for 30 kDa TNF inhibitor. The 30 kDa
CC TNF inhibitor can inhibit TNF alpha.
XX
SQ Sequence 455 AA;

Query Match 99.0%; Score 1219; DB 22; Length 455;
Best Local Similarity 100.0%; Pred. No. 2e-91;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 MGLSTVPDLLLLPLVLELLLVGIPSGVIGLPHLGDRKRDSCVCQGKYIHPPQNNSICT 60
Db 1 mglstvpdlllplvlllellvgipsgviglphlgdrkrdscvcqgkyihpqnnisict 60
QY 61 KCHKGYLYNDPCPGQQDDTDCRECSGSFTASENHLRCLSCSKCKEMGOVEISSCTWD 120
Db 61 khkgtylyndcpgpgqqddtcrecesgsftasenhlrlclscskckemgoveissctwd 120
QY 121 RDTVCGRKNQRYHYWSENLFQCFNCSLCNGTVHLSCOEKONTVCTCHAGFFLENECV 180
Db 121 rdtvcgrknqryhywsenlfqcfncslcngtvhlscoekqntvtctchagfflenecv 180
QY 181 SCSNCKSLECTKLCPQLPIENVKGTSDSTVTLLPLV 217
Db 181 scsnckslectklcpqlpienvkgtsdstvtllplv 217

Search completed: August 14, 2001, 05:36:42
Job time: 519 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2001, 05:31:58 ; Search time 13.45 Seconds
(without alignments)
335.263 Million cell updates/sec

Title: US-09-599-400A-9
Perfect score: 1231
Sequence: 1 MGLSTVPDLLPLVLLLELV.....ENVKGTSDSGTTLPLVRP 219

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents,AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1219	99.0	280	3	US-08-974-022-46
2	1219	99.0	455	1	US-08-050-319B-25
3	1219	99.0	455	1	US-08-321-668-2
4	1219	99.0	455	1	US-08-837-941-2
5	1219	98.0	455	2	US-08-126-016-2
6	1219	99.0	455	2	US-08-465-982-25
7	1219	99.0	455	4	US-09-086-483A-5
8	1189	96.6	453	4	US-08-050-319B-48
9	1124	91.3	199	2	US-08-465-982-48
10	1124	91.3	199	2	US-08-804-166-8
11	992.5	80.6	336	4	US-08-910-991-8
12	992.5	80.6	336	4	US-08-804-166-6
13	979	79.5	285	4	US-08-910-991-6
14	979	79.5	285	4	US-08-050-319B-2
15	946	76.8	167	1	US-08-050-319B-57
16	946	76.8	167	2	US-08-465-982-2
17	946	76.8	167	2	US-08-465-982-57
18	946	76.8	167	2	US-08-219-237B-4
19	900	73.1	153	2	US-08-477-347-12
20	900	73.1	153	4	US-08-232-087A-10
21	873	70.9	154	2	US-08-050-319B-54
22	854.5	69.4	158	2	US-08-465-982-54
23	854.5	69.4	256	4	US-08-804-166-2
24	842.5	68.4	256	4	US-08-910-991-2
25	842.5	68.4	256	4	US-08-050-319B-52
26	840	68.2	153	2	US-08-465-982-52
27	840	68.2	153	2	US-08-465-982-52

28	840	68.2	157	1	US-08-050-319B-50	Sequence 50, Appl
29	840	68.2	157	2	US-08-465-982-50	Sequence 50, Appl
30	837	68.0	307	4	US-08-804-166-4	Sequence 4, Appl
31	837	68.0	307	4	US-08-910-991-4	Sequence 4, Appl
32	731	59.4	124	1	US-08-050-319B-4	Sequence 4, Appl
33	731	59.4	124	2	US-08-465-982-4	Sequence 4, Appl
34	357	29.0	62	3	US-08-904-446A-17	Sequence 17, Appl
35	249	20.2	40	1	US-08-050-319B-26	Sequence 26, Appl
36	249	20.2	40	2	US-08-465-982-26	Sequence 26, Appl
37	245	19.9	41	1	US-08-050-319B-36	Sequence 36, Appl
38	245	19.9	41	2	US-08-465-982-36	Sequence 36, Appl
39	237	19.3	43	1	US-08-050-319B-31	Sequence 31, Appl
40	237	19.3	43	2	US-08-465-982-31	Sequence 31, Appl
41	220	17.9	39	1	US-08-050-319B-40	Sequence 40, Appl
42	220	17.9	39	2	US-08-465-982-40	Sequence 40, Appl
43	216.5	17.6	428	4	US-08-815-469-2	Sequence 2, Appl
44	210.5	17.1	197	2	US-08-505-606-1	Sequence 1, Appl
45	208	16.9	417	4	US-08-815-469-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-974-022-46
; Sequence 46, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-46

Query Match 99.0%; Score 1219; DB 3; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.2e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLPLVLLLELVGIVPSGVIGLPHLDREKRSVCPQGYIHPQNNISICT 60
DB 1 MGLSTVPDLLPLVLLLELVGIVPSGVIGLPHLDREKRSVCPQGYIHPQNNISICT 60

QY 61 KCHKTYLYNDPCPGQDTCRECSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
|||||
Db 61 KCHKTYLYNDPCPGQDTCRECSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
|||||
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
|||||
Db 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
|||||
QY 181 SC SNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||
Db 181 SC SNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||
RESULT 2
US-08-050-319B-25
; Sequence 25, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050.319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-25
Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
|||||
Db 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
|||||
QY 61 KCHKTYLYNDPCPGQDTCRECSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
|||||
Db 61 KCHKTYLYNDPCPGQDTCRECSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
|||||
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
|||||
Db 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
|||||
QY 181 SC SNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||
Db 181 SC SNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||

Db 181 SC SNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||
RESULT 3
US-08-321-668-2
; Sequence 2, Application US/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-321-668-2
Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
|||||
Db 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60
|||||
QY 61 KCHKTYLYNDPCPGQDTCRECSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
|||||
Db 61 KCHKTYLYNDPCPGQDTCRECSGFTASENHLRHCLSCSKCKRMKGQVEISSCTVD 120
|||||
QY 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
|||||
Db 121 RDTVCGCRKNQYRHYWSENLFQCFNCSCLNGTVHLSCQEKQNTVCTCHAGFFLRENECV 180
|||||
QY 181 SC SNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||
Db 181 SC SNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
|||||

RESULT 4
US-08-837-941-2
; Sequence 2, Application US/08837941
; Patent No. 5766917
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEEV, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,941
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/321,668
; FILING DATE: 12-OCT-1994
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-837-941-2

Query Match 99.0%; Score 1219; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.le-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPGKYIHPQNNISICT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPGKYIHPQNNISICT 60
QY 61 KCHKGTYLNDPCPGQDTCRECESSGFTASENHLRHLCLSCSKCKEMQGVIESSCTVD 120
DB 61 KCHKGTYLNDPCPGQDTCRECESSGFTASENHLRHLCLSCSKCKEMQGVIESSCTVD 120
QY 121 RDTVCGCRKNQYHYWSENLFQCFNCSLCINGTVHLSCKQKNTVCTCHAGFFLRENECV 180
DB 121 RDTVCGCRKNQYHYWSENLFQCFNCSLCINGTVHLSCKQKNTVCTCHAGFFLRENECV 180
QY 181 SCSCNCKKSLCTKLCPLQIENVKGTEDSGTIVLLPLV 217
DB 181 SCSCNCKKSLCTKLCPLQIENVKGTEDSGTIVLLPLV 217

RESULT 5
US-08-126-016-2

; Sequence 2, Application US/08126016
; Patent No. 5811261
; GENERAL INFORMATION:
; APPLICANT: WALLACH, DAVID
; APPLICANT: NOPHAR, YARON
; APPLICANT: KEMPER, OLIVER
; APPLICANT: ENGELMANN, HARTMUT
; APPLICANT: BRAKEBUSCH, CORD
; APPLICANT: ADERKA, DAN
; TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,016
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/625668
; FILING DATE: 13-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-126-016-2

Query Match 99.0%; Score 1219; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.le-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPGKYIHPQNNISICT 60
DB 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPGKYIHPQNNISICT 60
QY 61 KCHKGTYLNDPCPGQDTCRECESSGFTASENHLRHLCLSCSKCKEMQGVIESSCTVD 120
DB 61 KCHKGTYLNDPCPGQDTCRECESSGFTASENHLRHLCLSCSKCKEMQGVIESSCTVD 120
QY 121 RDTVCGCRKNQYHYWSENLFQCFNCSLCINGTVHLSCKQKNTVCTCHAGFFLRENECV 180
DB 121 RDTVCGCRKNQYHYWSENLFQCFNCSLCINGTVHLSCKQKNTVCTCHAGFFLRENECV 180
QY 181 SCSCNCKKSLCTKLCPLQIENVKGTEDSGTIVLLPLV 217
DB 181 SCSCNCKKSLCTKLCPLQIENVKGTEDSGTIVLLPLV 217

RESULT 6
US-08-465-982-25
; Sequence 25, Application US/08465982-
; Patent No. 5863786

GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
TITLE OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robbins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-982-25

Query Match 99.0%; Score 1219; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDREKRDVCPQGYIHPQNNISICT 60
DB 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDREKRDVCPQGYIHPQNNISICT 60
QY 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCLSCSKCKEMQVEISSCTVD 120
DB 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCLSCSKCKEMQVEISSCTVD 120
QY 121 RDTVCGRKNQRYHWSNLFQCFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
DB 121 RDTVCGRKNQRYHWSNLFQCFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
QY 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
DB 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217

RESULT 7
US-08-465-982-25
Sequence 5, Application US/08815469
Patent No. 6153402
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-815-469-5
Query Match 99.0%; Score 1219; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-101;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDREKRDVCPQGYIHPQNNISICT 60
DB 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLPHLGDREKRDVCPQGYIHPQNNISICT 60
QY 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCLSCSKCKEMQVEISSCTVD 120
DB 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCLSCSKCKEMQVEISSCTVD 120
QY 121 RDTVCGRKNQRYHWSNLFQCFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
DB 121 RDTVCGRKNQRYHWSNLFQCFNCSLCLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
QY 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
DB 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217
RESULT 8
US-09-086-483A-5
Sequence 5, Application US/09086483A
Patent No. 6214580
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,483A
FILING DATE: May-29-98

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/050,936

FILING DATE: May-30-97

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/069,112

FILING DATE: Dec-9-97

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ANDERS A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF379

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 453 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-086-483A-5

Query Match 96.6%; Score 1189; DB 4; Length 453;
Best Local Similarity 99.1%; Pred. No. 9.9e-99;
Matches 215; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60

Db 1 MGLSTVPDLLPLV-LELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHP-NNISICT 58

QY 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCSCKRKMGOVEISSCTVD 120

Db 59 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCSCKRKMGOVEISSCTVD 118

QY 121 RDTVCGCRKNQRYHWSLENLFCFNCISLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 180

Db 119 RDTVCGCRKNQRYHWSLENLFCFNCISLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 178

QY 181 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 217

Db 179 SCSNCKKSLCTKLCPLQIENVKGTEDSGTTVLLPLV 215

RESULT 9

US-08-050-319B-48

Sequence 48, Application US/08050319B

Patent No. 5633145

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robbins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-319B-48

Query Match 91.3%; Score 1124; DB 1; Length 199;
Best Local Similarity 99.5%; Pred. No. 2.6e-93;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60

Db 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT 60

QY 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCSCKRKMGOVEISSCTVD 120

Db 61 KCHKGTLYNDPCPGQDTCRECSGSFTASENHLRHLCSCKRKMGOVEISSCTVD 120

QY 121 RDTVCGCRKNQRYHWSLENLFCFNCISLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 180

Db 121 RDTVCGCRKNQRYHWSLENLFCFNCISLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 180

QY 181 SCSNCKKSLCTKLCPLQI 199

Db 181 SCSNCKKSLCTKLCPLQI 199

RESULT 10

US-08-465-982-48

Sequence 48, Application US/08465982

Patent No. 5663786

GENERAL INFORMATION:

APPLICANT: M.Feldmann, P.W. Gray,

APPLICANT: M.J.C. Turner, F.M. Brennan

TITLE OF INVENTION: Modified human TNFalpha (Tumor

TITLE OF INVENTION: Necrosis Factor alpha) Receptor

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Reed & Robbins

STREET: 635 Bryant Street

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Robert L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-982-48

Query Match 91.3%; Score 1124; DB 2; Length 199;
Best Local Similarity 99.5%; Pred. No. 2.6e-93;
Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLPLVLELVGYPGIVGLPHLGRDRKDSVCPQKGYTHPQNNSTCT 60
Db 1 MGLSTVPDLLLPLVLELVGYPGIVGLPHLGRDRKDSVCPQKGYTHPQNNSTCT 60
QY 61 KCHKGTYLNDPCPGQDTCRECESSFTASENHLRHCLSCSKCRKEMQVEISSCTVD 120
Db 61 KCHKGTYLNDPCPGQDTCRECESSFTASENHLRHCLSCSKCRKEMQVEISSCTVD 120
QY 121 RTVCGCRKNQRYHWSENLFCQFNCSLCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
Db 121 RTVCGCRKNQRYHWSENLFCQFNCSLCLNGTVHLSQCKQNTVCTCHAGFFLRENECV 180
QY 181 SCSNCKKSLECTKLCPLQI 199
Db 181 SCSNCKKSLECTKLCPLQI 199

RESULT 11
US-08-804-166-8
; Sequence 8, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; PRIOR APPLICATION NUMBER: 60/011,936
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-804-166-8o

Query Match 80.6%; Score 992.5; DB 4; Length 336;
Best Local Similarity 96.7%; Pred. No. 2.4e-81;
Matches 174; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 41 DSVCPQKGYTHPQNNSTCTCKCHKGTLYLNDPCPGQDTCRECESSFTASENHLRHCL 100
Db 23 DSVCPQKGYTHPQNNSTCTCKCHKGTLYLNDPCPGQDTCRECESSFTASENHLRHCL 82
QY 101 SCSKCRKEMQVEISSCTVDRTVCGCRKNQRYHWSENLFCQFNCSLCLNGTVHLSQCE 160
Db 83 SCSKCRKEMQVEISSCTVDRTVCGCRKNQRYHWSENLFCQFNCSLCLNGTVHLSQCE 142
QY 161 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCPLQIENVKGTEDSGTTV-LPLVLP 219
Db 143 KQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCPLQIENVKGTEDSGTTAGAGPRCP 202

RESULT 12
US-08-910-991-8
; Sequence 8, Application US/08910991
; Patent No. 6194177
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,991
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE: 20 February 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,936
; FILING DATE: 20 February 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: CAMPBELL-2B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
```

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-991-8

Query Match 80.6%; Score: 992.5; DB 4; Length 336;
Best Local Similarity 96.7%; Pred. No. 2.4e-81;
Matches 174; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 41 DSVCPQGYIHPQNNISICCTKCHGTYLYNDPCPGQDTCRECSGFTASENHLRCL 100
DB 23 DSVCPQGYIHPQNNISICCTKCHGTYLYNDPCPGQDTCRECSGFTASENHLRCL 82
QY 101 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160
DB 83 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 142
QY 161 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIENVKGTEDSGTTV-LLPLVRP 219
DB 143 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIENVKGTEDSGTTAGAGPRCP 202

RESULT 13

US-08-804-166-6
Sequence 6, Application US/08804166
Patent No. 6193972
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,166
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELL-2A
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-804-166-6

Query Match 79.5%; Score 979; DB 4; Length 285;

Best Local Similarity 98.8%; Pred. No. 3.3e-80;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 41 DSVCPQGYIHPQNNISICCTKCHGTYLYNDPCPGQDTCRECSGFTASENHLRCL 100
DB 23 DSVCPQGYIHPQNNISICCTKCHGTYLYNDPCPGQDTCRECSGFTASENHLRCL 82
QY 101 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160
DB 83 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 142
QY 161 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIENVKGTEDSGTT 211
DB 143 KONTVCTCHAGFFLRENECVSCSNCKKSLCTKLCPLQIENVKGTEDSGTT 193

RESULT 14

US-08-910-991-6
Sequence 6, Application US/08910991
Patent No. 6194177
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Jameson, Bradford A.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL-2B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-991-6

Query Match 79.5%; Score 979; DB 4; Length 285;

Best Local Similarity 98.8%; Pred. No. 3.3e-80;
Matches 169; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 41 DSVCPQGYIHPQNNISICCTKCHGTYLYNDPCPGQDTCRECSGFTASENHLRCL 100
DB 23 DSVCPQGYIHPQNNISICCTKCHGTYLYNDPCPGQDTCRECSGFTASENHLRCL 82
QY 101 SCSKCRKEMGOVEISSCTVDRDTCVCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSQOE 160

Db 83 SCCKRKGQVEISSCTVDRVTCGRKNQRYHWSENLFOCFNCTCLNGTVHLSQVE 142
QY 161 KQNTVCTCHAGFFLENECVSCSNCKKSLKCLPQIENVKGTEDSGTT 211
Db 143 KQNTVCTCHAGFFLENECVSCSNCKKSLKCLPQIENVKGTEDSGTT 193

RESULT 15

US-08-050-319B-2
; Sequence 2, Application US/08050319B
; Patent No. 5633145
; GENERAL INFORMATION:
; APPLICANT: M.Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319B
; FILING DATE: 10-May-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-050-319B-2

Query Match 76.8%; Score 946; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.6e-77;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTVPDLLPLVLELVGVPSCVIGLVPHLGDREKRDVCPQGYHPQNNISICT 60
Db 1 MGLSTVPDLLPLVLELVGVPSCVIGLVPHLGDREKRDVCPQGYHPQNNISICT 60
QY 61 KCHKGTLYLNDPCPGQDTCRECSGFTASENHLRHCLSCSKRCKEMQGVESISCTVD 120
Db 61 KCHKGTLYLNDPCPGQDTCRECSGFTASENHLRHCLSCSKRCKEMQGVESISCTVD 120
QY 121 RDTVCGCRKNQRYHWSENLFOCFNCSLCLNGTVHLSQVEKQNTVCT 167
Db 121 RDTVCGCRKNQRYHWSENLFOCFNCSLCLNGTVHLSQVEKQNTVCT 167

Search completed: August 14, 2001, 05:37:07
Job time: 309 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2001, 05:36:18 ; Search time 8.9 Seconds
(without alignments)
842.916 Million cell updates/sec

Title: US-09-599-400A-9

Perfect score: 1231

Sequence: 1 MGLSTVPDLLPLVLELLV.....ENVKGTEDSGTLLPLVRP 219

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1219	99.0	455	1	TNR1_HUMAN	P19438 homo sapien
2	906.5	73.6	461	1	TNR1_PIG	P50555 sus scrofa
3	879.5	71.4	454	1	TNR1_MOUSE	P22118 mus musculus
4	867	70.4	461	1	TNR1_RAT	P22934 rattus norv
5	859.5	69.8	471	1	TNR1_BOVIN	O19131 bos taurus
6	216.5	17.6	435	1	TNR1_HUMAN	P36941 homo sapien
7	208	16.9	417	1	WSL1_HUMAN	Q93038 h wsl-1 pro
8	202	16.4	427	1	NGFR_HUMAN	P08138 homo sapien
9	200	16.2	326	1	VT2_MXVL	P29825 myxoma viru
10	189	15.4	325	1	VT2_SFVKA	P25943 Shope fibro
11	188	15.3	425	1	NGFR_RAT	P07174 rattus norv
12	186.5	15.2	332	1	FASA_PIG	O77736 sus scrofa
13	181.5	14.7	415	1	TNR2_MOUSE	P50284 mus musculus
14	181	14.7	474	1	TNR2_MOUSE	P25119 mus musculus
15	180.5	14.7	327	1	FASA_MOUSE	P25446 mus musculus
16	174	14.1	289	1	CD40_MOUSE	P27512 mus musculus
17	172	14.0	269	1	CD40_BOVIN	Q28203 bos taurus
18	166.5	13.5	323	1	FASA_BOVIN	P51867 bos taurus
19	164	13.3	349	1	VC22_VARV	P34015 variola vir
20	162.5	13.2	461	1	TNR2_HUMAN	P20333 homo sapien
21	159.5	13.0	416	1	NGFR_CHICK	P18519 gallus gall
22	153.5	12.5	324	1	FASA_RAT	Q63199 rattus norv
23	148	12.0	277	1	CD40_HUMAN	P25942 homo sapien
24	143.5	11.7	1680	1	FUR2_DROME	P30432 drosophila
25	143	11.6	250	1	CD27_MOUSE	P41272 mus musculus
26	140	11.4	687	1	VS41_GIALA	P92127 giardia lam
27	138.5	11.3	260	1	CD27_HUMAN	P26842 homo sapien
28	137.5	11.2	335	1	FASA_MOUSE	P25445 homo sapien
29	137.5	11.2	1877	1	PK5_MOUSE	Q04592 mus musculus
30	135.5	11.0	595	1	CD30_HUMAN	P28908 homo sapien
31	135.5	11.0	1696	1	PK5_BACUL	Q9n115 branchiosto
32	135	11.0	272	1	OX40_MOUSE	P47741 mus musculus
33	132	10.7	913	1	PK5_HUMAN	Q92824 homo sapien

ALIGNMENTS

RESULT 1	TNR1_HUMAN	STANDARD;	PRT;	455 AA.
ID	TNR1_HUMAN	STANDARD;	PRT;	455 AA.
AC	P19438;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 1) (TBPI) (P60) (TNF-R1) (TNF-R1) (P55) (CD120A).			
GN	TNFRSF1A OR TNFR1 OR TNFR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=90235285; PubMed=2158863;			
RA	Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Getanaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;			
RT	"Molecular cloning and expression of a receptor for human tumor necrosis factor.";			
RL	Cell 61:361-370(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90235284; PubMed=2158862;			
RA	Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M., Tabuchi H., Lesslauer W.;			
RT	"Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.";			
RL	Cell 61:351-359(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.			
RX	MEDLINE=91006021; PubMed=1698610;			
RA	Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwang R., Aderka D., Hollmann H., Wallach D.;			
RT	"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor.";			
RL	EMBO J. 9:3269-3278(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91090841; PubMed=1702293;			
RA	Himmeler A., Maurer-Foxy I., Kroenke M., Scheurich P., Pfizenmaier K., Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;			
RT	"Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.";			
RL	DNA Cell Biol. 9:705-715(1990).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Placenta;			
RC	MEDLINE=91017509; PubMed=2170974;			
RX	Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;			
RT	"Cloning of human tumor necrosis factor (TNF) receptor cDNA and			

34	130.5	10.6	3672	1	LML2_CAREL	Q21313 caenorhabdi
35	126.5	10.3	271	1	OX40_RAT	P15725 rattus norv
36	124.5	10.1	277	1	OX40_HUMAN	P43489 homo sapien
37	119	9.7	279	1	SLI3_MOUSE	O70433 mus musculus
38	119	9.7	2318	1	NTC3_MOUSE	O61982 mus musculus
39	118	9.6	1790	1	LMB1_DROME	P11046 drosophila
40	117	9.5	1712	1	TGFB_RAT	Q00918 rattus norv
41	116.5	9.5	892	1	LDL2_XENLA	Q99088 xenopus lae
42	116	9.4	279	1	SLI3_RAT	O35115 rattus norv
43	116	9.4	898	1	ZO71_XENLA	P18751 xenopus lae
44	115.5	9.4	667	1	TS11_GIALA	Q03185 giardia lam
45	115	9.3	279	1	SLI3_HUMAN	Q14192 homo sapien

expression of recombinant soluble TNF-binding protein.";
 [6] Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
 RP MEDLINE-92250049; PubMed-131517;
 RA Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;
 RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and
 RT localization to chromosome 12p13.";
 RL Genomics 13:219-224(1992).
 [7]
 RP SEQUENCE OF 41-45.
 RX MEDLINE-90110215; PubMed-2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface
 RT tumor necrosis factor receptors.";
 RL J. Biol. Chem. 265:1531-1536(1990).
 [8]
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.
 RX MEDLINE-93258809; PubMed-8387891;
 RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
 RA Broger C., Loetscher H., Lesslauer W.;
 RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
 RT beta complex: implications for TNF receptor activation.";
 RL Cell 73:431-445(1993).
 [9]
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
 RX MEDLINE-97094982; PubMed-8939750;
 RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;
 RT "Structures of the extracellular domain of the type I tumor necrosis
 RT factor receptor.";
 RL Structure 4:1251-1262(1996).
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF
 CC NONCYTOTOXIC TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION
 CC OF THE ACID SPHINGOMYELINASE.
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -!- SIMILARITY: CONTAINS A DEATH DOMAIN.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X55313; CAA39021.1; -
 DR EMBL; M33294; AAA03210.1; -
 DR EMBL; M58286; AAA36753.1; -
 DR EMBL; M63121; AAA36754.1; -
 DR EMBL; M75866; AAA61201.1; -
 DR EMBL; M75864; AAA61201.1; JOINED.
 DR EMBL; M75865; AAA61201.1; JOINED.
 DR EMBL; M60275; AAA36756.1; -

DR EMBL; A21522; CAA01558.1; -
 DR PIR; A34899; GQHUT1.
 DR PIR; A35010; A35010.
 DR PIR; S12057; S12057.
 DR PIR; A38208; A38208.
 DR PDB; 1TNR; 31-JUL-94.
 DR PDB; 1NCF; 07-DEC-95.
 DR PDB; 1EXT; 11-JAN-97.
 DR MIM; 191190; -
 DR InterPro; IPR000488; -
 DR InterPro; IPR001388; -
 DR Pfam; PF00020; TNFR_c6; 4.
 DR Pfam; PF00531; death; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00500; TNFR_NGFR_2; 3.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;
 KW 3D-structure.
 KW SIGNAL 1 21
 FT CHAIN 22 455 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT CHAIN 41 291 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
 FT DOMAIN 22 211 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 234 POTENTIAL.
 FT DOMAIN 235 455 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 196 4 X TNFR-CYS.
 FT REPEAT 43 82 TNFR-CYS 1.
 FT REPEAT 83 125 TNFR-CYS 2.
 FT REPEAT 126 166 TNFR-CYS 3.
 FT REPEAT 167 196 TNFR-CYS 4.
 FT DOMAIN 338 348 N-SMASE ACTIVATION DOMAIN (NSD).
 FT DOMAIN 356 441 DEATH DOMAIN.
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 412 412 MISSING (IN REF. 4).
 FT CONFLICT 443 446 GPAA -> APP (IN REF. 4).
 SQ SEQUENCE 455 AA; 50494 MW; 4CEPBA96D03B8225 CRC64;

Query Match 99.0%; Score 1219; DB 1; Length 455;
 Best Local Similarity 100.0%; Pred. No. 3.1e-95;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYTHPQNNISCTT 60
 DB 1 MGLSTVPDLLLPLVLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYTHPQNNISCTT 60
 QY 61 KCHKGYLYNDPCPGQDTCRECEGSFTASENHLRHCLSCSKRKMGMQVEISSCTVD 120
 DB 61 KCHKGYLYNDPCPGQDTCRECEGSFTASENHLRHCLSCSKRKMGMQVEISSCTVD 120
 QY 121 RDTVCGRKNQYRHYWSENFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 180
 DB 121 RDTVCGRKNQYRHYWSENFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFFLRENECV 180
 QY 181 SCSCNCKKSLCTKLCPLQIENVGKTEDSGTTVLLPLV 217
 DB 181 SCSCNCKKSLCTKLCPLQIENVGKTEDSGTTVLLPLV 217

RESULT 2

TNRL_PIG
ID TNRL_PIG STANDARD; PRT; 461 AA.
AC P50555;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1) (P55).
GN TNFRSF1A OR TNFR1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=96011645; PubMed=7590278;
RA Suter B., Pauli U.H.;
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.";
RL Gene 163:263-266(1995).
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U19994; AAC48499.1; -
DR HSSP; P19438; 1TNFR.
DR InterPro; IPR000488; -
DR InterPro; IPR001368; -
DR Pfam; PF00020; TNFR_c6; 3.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT SIGNAL 1 21
FT CHAIN 22 461
FT DOMAIN 22 210
FT TRANSMEM 211 233
FT DOMAIN 234 461
FT DOMAIN 43 195
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 195
FT REPEAT 340 350
FT DOMAIN 362 447
FT DOMAIN 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99

FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 190 BY SIMILARITY.
FT DISULFID 185 194 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 73.6%; Score 906.5; DB 1; Length 461;
Best Local Similarity 74.7%; Pred. No. 4.7e-69;
Matches 162; Conservative 16; Mismatches 38; Indels 1; Gaps 1;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDRKRSVCPQGYIHPQNNISICT 60
Db 1 MGLSTVPGLLLPLVLRALLVDVYAGVHGLVHPGDKRESLCPQGYKSHYPQNRISICT 60
QY 61 KCHKGTLYNDPCPGQDTCRECSGTSASENHLRHLCSCKRCKEMGQVEISSCTVD 120
Db 61 KCHKGTLYLHNDCLGPDTCRECDNGTTFASENHLTQCLSCSKRSEMSQVEISPTVD 120
QY 121 RDTVCGGRKNQRYHWSENLFCQFCNCSLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
Db 121 RDTVCGGRKNQRYHWSENLFCQFCNCSLNGTVHLSQEKQNTVCTCHAGFFLRENECV 180
QY 181 SCSCNCKSLECKLCPQIENVKGTEDSGTVLLPLV 217
Db 181 SCVCKNA-DCKNLCPATSETRNDFQDTGTVLLPLV 216

RESULT 3
TNRL_MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1) (P55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91187885; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.X., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor.";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91285014; PubMed=1647956;
RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,
RA Gray P.W., Feldmann M., Foxwell B.M.J.;
RT "Cloning, expression and cross-linking analysis of the murine p55

tumor necrosis factor receptor.";
 Eur. J. Immunol. 21:1649-1656(1991).
 [4]
 RN SEQUENCE FROM N.A.
 RC TISSUE-Spleen;
 RX MEDLINE=92039815; PubMed=1657766;
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:338-340(1991).
 [5]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94245292; PubMed=8188324;
 RX Bebo B.F., Linthicum D.S.;
 RA "Nucleotide sequence of the TNF type I receptor from a mouse
 endothelioma cell line.";
 RT Immunogenetics 39:450-451(1994).
 [6]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93156721; PubMed=8381516;
 RX Rothe J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RA "Genomic organization and promoter function of the murine tumor
 necrosis factor receptor beta gene.";
 RT Mol. Immunol. 30:165-175(1993).
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFRI LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFRI COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; M60468; AAA39751.1; -
 DR EMBL; M59377; AAA40464.1; -
 DR EMBL; X59238; CAA41922.1; -
 DR EMBL; X57796; CAA40936.1; -
 DR EMBL; L26349; AAA59361.1; -
 DR EMBL; M76656; AAA40465.1; -
 DR EMBL; M8067; AAA40465.1; JOINED.
 DR EMBL; M76655; AAA40465.1; JOINED.
 DR PIR; A38634; GQMST1.
 DR PIR; S16677; S16677.
 DR PIR; S19021; S19021.
 DR HSSP; P19438; 1EXT.
 DR MGD; MGI:1314884; Tnfrsf1a.
 DR InterPro; IPR000488; -
 DR InterPro; IPR001368; -
 DR Pfam; PF00020; TNFR_c6; 4.
 DR Pfam; PF00531; Death; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00505; TNFR_NGFR_2; 3.
 DR PROSITE; PS00017; DEATH_DOMAIN; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.
 FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	213	235	POTENTIAL.
FT DOMAIN	236	454		CYTOPLASMIC (POTENTIAL).
FT DOMAIN	43	196		4 X TNFR-CYS.
FT REPEAT	43	82		TNFR-CYS 1.
FT REPEAT	83	125		TNFR-CYS 2.
FT REPEAT	126	166		TNFR-CYS 3.
FT REPEAT	167	196		TNFR-CYS 4.
FT DOMAIN	339	349		N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN	356	441		DEATH DOMAIN.
FT DISULFID	44	58		BY SIMILARITY.
FT DISULFID	59	72		BY SIMILARITY.
FT DISULFID	62	81		BY SIMILARITY.
FT DISULFID	84	99		BY SIMILARITY.
FT DISULFID	102	117		BY SIMILARITY.
FT DISULFID	105	125		BY SIMILARITY.
FT DISULFID	127	143		BY SIMILARITY.
FT DISULFID	146	158		BY SIMILARITY.
FT DISULFID	149	166		BY SIMILARITY.
FT DISULFID	168	179		BY SIMILARITY.
FT DISULFID	182	191		BY SIMILARITY.
FT DISULFID	185	195		BY SIMILARITY.
FT CARBOHYD	54	54		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	151	151		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	202	202		N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT	394	394		R -> G (IN REF. 6).
SQ SEQUENCE	454 AA;	50129 MW;	0710C2B8C3C2B6D9 CRC64;	

Query Match 71.4%; Score 879.5; DB 1; Length 454;
 Best Local Similarity 71.6%; Pred. No. 8.4e-67;
 Matches 156; Conservative 23; Mismatches 38; Indels 1; Gaps 1;

QY	1	MGLSTVPDLLLPLVLELLVIGVPSGVLPHGLDREKDSVCPQGGKYHPQNNISCTT	60
DB	1	MGLTVPGLLLSLALLLGIHPSGVTGLVPSLGLDREKDSVCPQGGKYHSHKNSICTT	60
QY	61	KCHKGYLVNDPCPGQDTCRECSGTFASENHLRHLCSCKRKGVEISSCTVD	120
DB	61	KCHKGYLVSDCPGPRDTCRECEKGTFTASQNYLRQCLSKCTCKREMSQVLSPOAD	120
QY	121	RDTVCCKRKNQRYHWSNLFQCFNCSCLNGTVHLSCQKQNTVCTCHAGFFLRENECV	180
DB	121	KDFVCGCKENQFQYLSETHFQVDCSPCFNGTWTIPCKETQNTVCNCHAGFFLRESECV	180
QY	181	SCSNCKRKSLECTKLCL-PQIENVKGTEDSGTTVLLPLV	217
DB	181	PCSHCKKNEECMKLCLPPLANVTNPQDSGTAVLLPLV	218

RESULT 4
 TNRI_RAT ID TNRI_RAT STANDARD; PRT; 461 AA.
 AC P22934;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-RI) (TNF-RI) (P55).
 DE (P55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91090841; PubMed=1702293;
 RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
 RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
 RT "Molecular cloning and expression of human and rat tumor necrosis
 RT factor receptor chain (p60) and its soluble derivative, tumor
 RT necrosis factor-binding protein.";
 RL DNA Cell Biol. 9:705-715(1990).
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD

CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY)
 CC
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M63122; AAA42256.1; -;
 CC PIR; B36555; B36555.
 CC HSSP; P19438; 1TNR.
 CC InterPro; IPR000488; -;
 CC InterPro; IPR001368; -;
 CC Pfam; PF00020; TNFR_c6; 4.
 CC Pfam; PF00531; death; 1.
 CC PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC PROSITE; PS00500; TNFR_NGFR_2; 3.
 CC PROSITE; PS50017; DEATH_DOMAIN; 1.
 CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 KW SIGNAL 1 21
 FT CHAIN 22 461
 FT DOMAIN 212 234
 FT TRANSMEM 212 234
 FT DOMAIN 235 461
 FT DOMAIN 43 196
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 344 354
 FT DOMAIN 363 448
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 151 151
 FT CARBOHYD 201 201
 SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;

Query Match 70.4%; Score 867; DB 1; Length 461;
 Best Local Similarity 70.0%; Pred. No. 9.5e-66;
 Matches 152; Conservative 21; Mismatches 44; Indels 0; Gaps 0;

QY 1 MGLSTVPLDLLPLVLELLVIGPSGVIGVPHLGDREKRDVCPQCKYTHPQNNISCTCT 60
 DB 1 MGLPIVGLLSLLVLLALLMGIHPGVTLVPSLGDREKRDNLCPQCKYAHPRNNSICT 60

QY 61 KCHKGTYLYNDPCPGQDTCDCRECEGSFTASENHLRHLCSCKRKEMQVEISCTVD 120
 DB 61 KCHKGTYLVSDPCSPGQETVCVCKGTFTASQNHVROCLSKCTCKRKEMQVEISPKAD 120
 QY 121 RDTVCGCRKNQYRHWSENLFQCFNCISCLNGTVHLSQEKONTVCTCHAGFLRENECV 180
 DB 121 MDTVCGCRKNQYRHWSENLFQCFNCISCLNGTVHLSQEKONTVCTCHAGFLRENECV 180
 QY 181 SCNCKKSLCTKLCPLQENNVKGTEDSGTTVLLPLV 217
 DB 181 PCSCKCKNQCKKLCPLPPVANNVTFNPDGTAVALPLV 217

RESULT 5

TNRI_BOVIN STANDARD; PRT: 471 AA.
 ID TNRI_BOVIN
 AC 019131;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-R1)
 DE (P55).
 GN TNFRSF1A OR TNFR1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RC Lee E.-K., Talyor M.J., Kehrli M.E.;
 RT "Cloning of cDNA encoding bovine tumor necrosis factor-receptor 1
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U09037; AAB65143.1; -;
 CC HSSP; P19438; 1TNR.
 CC InterPro; IPR000488; -;
 CC InterPro; IPR001368; -;
 CC Pfam; PF00020; TNFR_c6; 3.
 CC Pfam; PF00531; death; 1.
 CC PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC PROSITE; PS00500; TNFR_NGFR_2; 2.
 CC PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 FT SIGNAL 1 21
 FT CHAIN 22 461
 FT DOMAIN 212 234
 FT TRANSMEM 212 234
 FT DOMAIN 235 461
 FT DOMAIN 43 196
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 344 354
 FT DOMAIN 363 448
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 151 151
 FT CARBOHYD 201 201
 SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;

```

FT CHAIN 22 471 TUMOR NECROSIS FACTOR RECEPTOR 1.
FT DOMAIN 22 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 233 POTENTIAL.
FT DOMAIN 234 471 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 243 471 4 X TNFR-CYS.
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 195 TNFR-CYS 4.
FT DOMAIN 340 360 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 372 457 DEATH DOMAIN.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 82 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 190 BY SIMILARITY.
FT DISULFID 185 194 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 471 AA: 51367 MW; 5243EF514DFE81C4 CRC64;

Query Match 69.8%; Score 859.5; DB 1; Length 471;
Best Local Similarity 69.6%; Pred. No. 4.1e-65;
Matches 151; Conservative 22; Mismatches 43; Indels 1; Gaps 1;

QY 1 MGLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREKDSVCPQGYIHPONNSICT 60
DB 1 MGLTVPGLLLPLVLPALLADVPAGVGLVPHGDLKRESPCQGYIHPONNSICT 60

QY 61 KCHKGTLYNDPCPGQDQDRCESGSGFTASENHLRCLSCSKCRKEMGOVEISSCTVD 120
DB 61 KCHKGTLYNDPCPGQDQDRCVRCAGFTALENHLRCLSCRCRDEMFOVEISPCVD 120

QY 121 RDTVCGCRNQYRHYWSENLFQCFNCSLCLNGTGVHLSQEQKNTVCTCHAGFFLENQCV 180
DB 121 RDTVCGCRNQYRHYWSENLFQCFNCSLCLNGTGVHLSQEQKNTVCTCHAGFFLENQCV 180

QY 181 SCSNCKSKSECTKLCPLQIENVKGTEDSGTGVLLPLV 217
DB 181 SCHDCKNK-ECEKLCPTRPSTGKDSQDPGTGVLLPLV 216

RESULT 6
TNRC_HUMAN STANDARD; PRT: 435 AA.
AC P36941;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTBR OR TNFR OR TNFRSF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
RL transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
RN [2]

```

```

RP FUNCTION
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L04270; AAA36757.1; -.
DR HSSP: P25942; 1CDF.
DR MIM: 600979; -.
DR InterPro: IPR001368; -.
DR Pfam: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 435 LYMPHOTOXIN-BETA RECEPTOR.
FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 228 248 POTENTIAL.
FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 211 4 X TNFR-CYS.
FT REPEAT 42 81 TNFR-CYS 1.
FT REPEAT 82 124 TNFR-CYS 2.
FT REPEAT 125 168 TNFR-CYS 3.
FT REPEAT 169 211 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
FT DISULFID 104 124 BY SIMILARITY.
FT DISULFID 126 132 BY SIMILARITY.
FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 17.6%; Score 216.5; DB 1; Length 435;
Best Local Similarity 32.0%; Pred. No. 2.7e-11;
Matches 71; Conservative 23; Mismatches 103; Indels 25; Gaps 12;

QY 2 GLSTVPDLLPLVLELLVGIYPSGVIGLVPHLGDREK-RDSVCPQGYIHPONNSICT 60
DB 11 GLWGP---LVGLGLAASQPAQ---PPYASENQTCDQ---EKEYEPQHR-ICCS 60

QY 61 KCHKGTLYNDPCPGQDQDRCESGSGFTASENHLRCLSCSKCRKEMGOVEISSCTVD 120
DB 61 RCPPTVVSAC-SRIEDTVCAICAENSYNEHWNYLICQLCRPCDPVMGLEEAPCTSK 119

QY 121 RDTVCGCRNQYRHYWSENLFQCFNCSL---CLNGTVHLSQEQ---KONTVCT-CHAGFFL 174
DB 120 RKTQCRCPQGMFCAAWA---LECTHCELLSDCPPGTAEELKDEVGKGNHVCVPCKAGHF- 175

QY 175 RENEVCSNCKSKSECTKLCPLQIENVKGTEDSGTGVLLPL 216
DB 176 -QNTSSPASCQPHTRCENQGL--VEAAPTQASDITCKNPL 214

```


DT 15-JUL-1999 (Rel. 38, Last annotation update)
GN TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
OS Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=31530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91335768; PubMed=1651597;
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence.";
RL Virology 184:370-382(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M95181; AAA46632.1; -;
CC EMBL; A23729; CAA01688.1; -;
CC PIR; A40566; GQVZML.
CC HSSP; P19438; 1TNR.
CC InterPro: IPR001368; -;
CC Pfam: PF00020; TNFR_C6; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; Glycoprotein; Repeat; Signal.
CC SIGNAL 1 16 POTENTIAL.
CC CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
CC DOMAIN 27 186 4 X TNFR-CYS.
CC REPEAT 27 62 TNFR-CYS 1.
CC REPEAT 63 104 TNFR-CYS 2.
CC REPEAT 105 147 TNFR-CYS 3.
CC REPEAT 148 186 TNFR-CYS 4.
CC CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;
Query Match 16.2%; Score 200; DB 1; Length 326;
Best Local Similarity 25.8%; Pred. No. 5.1e-10;
Matches 62; Conservative 28; Mismatches 88; Indels 62; Gaps 10;
QY 14 VLELLGVIPSGVIGLVPHLGDREKRDSCVCPQGYIHPQNNISCTCKCHKGTLYNDGP 73
DB 6 LLLAYACVYGGG----APYGADRGK----CRGNDY---EKDGLCCSPGPGSVASRLC- 53
QY 74 GPQDQDCRECESGSFTASENHLRHCLSC-SKCRKEMGOVEISSCTVDRTVCGRNQY 132
DB 54 GPQSDTVCSCKNETFTASTNHAPACVSCRGRTGHLS--ESQSCDTRDRVDCSAGNY 111
QY 133 -----RHYSENLFQCFNCISCLNG- 152
DB 112 CLLKGQGCRCAPKTKCPAGYGVSHRTGDLVLTCKPRTYSDAVSSFTCTSSFNVI 171
QY 153 TVHLSQOEKQNTVCTCHAGFFLRENECVSCNCKSL---ECTKLCLPQINVRKGTDSG 209
DB 172 SVEFNLPVNDTCTTTAG----PNEVVKTSEFVTLNHTDCDPVFHTYYGTSSSEGAG 227
RESULT 10

VT2_SFVKA
ID VT2_SFVKA STANDARD; PRT; 325 AA.
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321103; PubMed=2820128;
RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT telomeric region of the Shope fibroma virus genome.";
RL Virology 160:20-30(1987).
RN [2]
RP FUNCTION.
RX MEDLINE=91207415; PubMed=1850261;
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "T2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M17433; -; NOT_ANNOTATED_CDS.
CC EMBL; A23727; CAA01687.1; -;
CC PIR; B43692; B43692.
CC HSSP; P19438; 1TNR.
CC InterPro: IPR001368; -;
CC Pfam: PF00020; TNFR_C6; 2.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 1.
CC Receptor; Glycoprotein; Repeat; Signal.
CC SIGNAL 1 16 POTENTIAL.
CC CHAIN 17 325 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
CC DOMAIN 27 186 4 X TNFR-CYS.
CC REPEAT 27 62 TNFR-CYS 1.
CC REPEAT 63 104 TNFR-CYS 2.
CC REPEAT 105 147 TNFR-CYS 3.
CC REPEAT 148 186 TNFR-CYS 4.
CC CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;
Query Match 15.4%; Score 189; DB 1; Length 325;
Best Local Similarity 27.7%; Pred. No. 4.2e-09;
Matches 57; Conservative 25; Mismatches 82; Indels 42; Gaps 10;
QY 9 LLLPLVLELLGVIPSGVIGLVPHLGDREKRDSCVCPQGYIHPQNNISCTCKCHKGTLYL 68
DB 1 MLRLTALLVCVVYVYGGD---VPYSSNQK---CGGHDY---EKDGLCCASCHPGFYA 49
QY 69 YNDGPGQDQDTCRECESGSFTASENHLRHCLSC-SKCRKEMGOVEISSCTVDRTVCGR 127

Db 50 SRLC-GPGSNTVCSPECDGTFSTASTNHAPACVSCRCPTGCHLS--ESQPCDRTHDRVNC 106
 QY 128 RKNQYRHYWSENLFQCNGLNCTVHLSCQEKQNTVCTCHAGFLRENECVSCSNCKK 187
 Db 107 STGNYCLLKGNQ-----GCRICAPQT-----KCPAGYGVSGHTRAGDTLCEK 148
 QY 188 SLECKLCLPQI--ENVKTEDSGIT 211
 Db 149 -----CPPHTYSDLSPTERCSTG 167
 RESULT 11
 NGFR_RAT STANDARD; PRT:- 425 AA.
 AC P07174;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LNGFR) (P75 ICD).
 GN NGFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87115859; PubMed=3027380;
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
 RT "Gene transfer and molecular cloning of the rat nerve growth factor
 RT receptor.";
 RL Nature 325:593-597(1987).
 [2]
 RN SEQUENCE OF 1-22 FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=93077038; PubMed=1446821;
 RA Metsis M., Timusk T., Allikmets R., Saarma M., Persson H.;
 RT "Regulatory elements and transcriptional regulation by testosterone
 RT and retinoic acid of the rat nerve growth factor receptor promoter.";
 RL Gene 121:247-254(1992).
 [3]
 RP STRUCTURE BY NMR OF 334-418.
 RX MEDLINE=9749145; PubMed=9305641;
 RA Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
 RL EMBO J. 16:4999-5005(1997).
 CC -!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -!- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 DR EMBL; X05137; CAA28783.1; -
 DR EMBL; X61269; -; NOT_ANNOTATED_CDS.
 DR PIR; A26431; A26431.
 DR PDB; INGR; 29-JUL-97.
 DR InterPro; IPR000488; -
 DR InterPro; IPR001368; -
 DR Pfam; PF00020; TNFR_c6; 4.
 DR Pfam; PF00531; death; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 4.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 FT SIGNAL 1 29
 FT CHAIN 30 425 LOW-AFFINITY NERVE GROWTH FACTOR
 FT RECEPTOR.
 FT DOMAIN 30 251 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 252 273 POTENTIAL.
 FT DOMAIN 274 425 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 190 4 X TNFR-CYS.
 FT REPEAT 32 66 TNFR-CYS 1.
 FT REPEAT 67 108 TNFR-CYS 2.
 FT REPEAT 109 148 TNFR-CYS 3.
 FT REPEAT 149 190 TNFR-CYS 4.
 FT DOMAIN 198 249 SER/THR-RICH.
 FT DOMAIN 354 419 DEATH DOMAIN.
 FT DISULFID 33 44 BY SIMILARITY.
 FT DISULFID 45 58 BY SIMILARITY.
 FT DISULFID 48 65 BY SIMILARITY.
 FT DISULFID 68 84 BY SIMILARITY.
 FT DISULFID 87 100 BY SIMILARITY.
 FT DISULFID 90 108 BY SIMILARITY.
 FT DISULFID 110 123 BY SIMILARITY.
 FT DISULFID 126 139 BY SIMILARITY.
 FT DISULFID 129 147 BY SIMILARITY.
 FT DISULFID 150 165 BY SIMILARITY.
 FT DISULFID 168 181 BY SIMILARITY.
 FT DISULFID 171 189 BY SIMILARITY.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;
 Query Match 15.3%; Score 188; DB 1; Length 425;
 Best Local Similarity 28.6%; Pred. No. 6.4e-09;
 Matches 58; Conservative 30; Mismatches 79; Indels 36; Gaps 12;
 QY 14 VLELLLVGYPGVIGLVPHLGDREKRDVCPQSKYIHPQNNISCTCKHKGTLYLNDP 73
 Db 16 LLLLLILGVSSGA-----KETCSTGLYTH---SGECCKACNLGEGVAQPC- 58
 QY 74 GPCQDTCREC-ESGFTASENHLRHLCSCKRKMGEVSEISS-CHVDRTVCGCRKNQ 131
 Db 59 GANQ-TVCEPCLNDFVSDVATPCPKCTEC---LGLQSMAPCVADDAVCRC---A 111
 QY 132 YRYWSENLPQCNCISCLNGT-VHLSCQEKQNTVC-TCHAGFLRE----NECVSCSN 185
 Db 112 YGIYDEETHCHCACSVCEVSGLVFSCQDKQNTVCCEPEGIYSDEANHVDPCLPTVC 171
 QY 186 ----KKSLECTKLCLPQIENVKG 204
 Db 172 EDTERQLRECTPWADAECEIIP 194
 RESULT 12
 FASA_PIG STANDARD; PRT; 332 AA.
 ID FASA_PIG
 AC 07736;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darner D.;
 RT "Expression of apoptosis-associated genes in hibernating and stunned
 RT myocardium of pig.";

RN [2]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=93189576; PubMed=7680478;
RA Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT "Aberrant transcription caused by the insertion of an early
TT transposable element in an intron of the Fas antigen gene of lpr
RT mice";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN [3]
RP VARIANT LPR.
RX MEDLINE=92195401; PubMed=1372394;
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Nagata S.;
RT "Lymphoproliferation disorder in mice explained by defects in Fas
RT antigen that mediates apoptosis";
RL Nature 356:314-317(1992).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC LIVER, LUNG, HEART, AND ADULT OVARY.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC PRODUCTION.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M83649; AAA37593.1; -;
DR EMBL; S56490; AAB25700.1; -;
DR EMBL; S56485; AAB25700.1; JOINED.
DR EMBL; S56486; AAB25700.1; JOINED.
DR PIR; A46484; A46484.
DR HSP; P25445; 1DDF.
DR MGD; MGI:95484; Fas.
DR InterPro; IPR000488; -;
DR InterPro; IPR001368; -;
DR Pfam; PF00020; TNFR_G6; 3.
DR Pfam; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
KW Disease mutation.
FT SIGNAL 1 21
FT CHAIN 22 327 FASL RECEPTOR.
FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 186 POTENTIAL.
FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 43 162 3 X TNFR-CYS.
FT REPEAT 43 79 TNFR-CYS 1.
FT REPEAT 80 123 TNFR-CYS 2.
FT REPEAT 124 162 TNFR-CYS 3.
FT REPEAT 222 306 DEATH DOMAIN.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 246 246 I -> N (IN LPR).
FT

SQ SEQUENCE 327 AA; 37418 MW; F6BFFC5ACE356EEE CRC64;
Query Match 14.7%; Score 180.5; DB 1; Length 327;
Best Local Similarity 25.9%; Pred. No. 2.2e-08;
Matches 55; Conservative 24; Mismatches 94; Indels 39; Gaps 7;
QY 10 LLPLVLELLVGIYPSGVIGLVPHLGDEK---RDSVCPQGYIHPQNNISICTYKCHGT 66
Db 7 VLPLVLAGSQLRVHTQGTNSISESLKLRVRRVHETDKNCSEGLY---QGGPFCCQCPQPK 63
QY 67 YLYNDGCPGQDTCRECESGSFTASENHLR-HCLSCSKCRKEMQVEISSCTVDRTVC 125
Db 64 KVEDCKMNGGTPTCAPCTEKEYMDKNHYADKRCRCRLCDDEEHGLEVETNCTLTQNTKC 123
QY 126 GCRKNQVRHYWSENLFQCFNCSLCLNGTVHLSQCEKQNTVCTCHAGFFELRENECVCSNC 185
Db 124 KCKPDFYCD--SPCEHCVRCAECHEGTLE-PCATATSN-----NC 161
QY 186 KKSLECTKLCPLQIENVKGTEDSGTTVLLPLV 217
Db 162 RKQSPRNLRLTLTI-----LVLLIPLV 183
Search completed: August 14, 2001, 05:38:27
Job time: 129 sec

file copy
Sequence
Comparison

RESULT 1
CQUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding prot
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 08-Dec-2000
C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; J10758; A60231;
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to
A:Reference number: A38208; MUID:92250049
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PI
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Less
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor re
A:Reference number: A34899; MUID:90235284
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOE>
A:Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A:Experimental source: Placenta
A:Note: part of this sequence, including the amino end of the mature protein, confirm
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga,
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis fact
A:Reference number: A34900; MUID:90235285
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A:Reference number: A36555; MUID:91090841
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HIM>
A:Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',16
R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A:Reference number: A38281; MUID:91017509
A:Accession: A38281
A:Molecule type: mRNA

A:Residues: 1-455 <GRA>
 A:Cross-references: GB:M37764
 A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
 R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
 EMBO J. 9, 3269-3278, 1990
 A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type
 le form of the receptor.
 A:Reference number: S12057; MUID:91006021
 A:Accession: S12057
 A:Molecule type: mRNA
 A:Residues: 1-455 <NOP>
 A:Cross-references: EMBL:X55133; NID:q37223; PIDN:CAA39021.1; PID:q37224
 A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, W
 R:Kemper, O.; Wallach, D.
 Gene 134, 209-216, 1993
 A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
 A:Reference number: JT0758; MUID:94085779
 A:Accession: JT0758
 A:Molecule type: DNA
 A:Residues: 1-13 <KEM>
 R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
 Eur. J. Immunol. 20, 1167-1174, 1990
 A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
 A:Reference number: A60231; MUID:90292116
 A:Accession: A60231
 A:Molecule type: protein
 A:Residues: 41-43, 'X', '45-53, 'X', '55-57 <SEC>
 R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
 Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
 A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
 tents.
 A:Reference number: A38258; MUID:91062364
 A:Accession: A38258
 A:Molecule type: protein
 A:Residues: 41-60 <GAR>
 A:Experimental source: cancer patient serum
 R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyse, H.; Grubb, A.; Adolf, G.
 Eur. J. Haematol. 42, 270-275, 1989
 A:Title: Isolation and characterization of a tumor necrosis factor binding protein from
 A:Reference number: A60594; MUID:89171156
 A:Accession: A60594
 A:Molecule type: protein
 A:Residues: 41-43, 'X', '45-53, 'V', '55-57, 'XK', '60 <OLS>
 A:Experimental source: renal failure patient urine
 R:Engelmann, H.; Novick, D.; Wallach, D.
 Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:90110215
 A:Accession: A35010
 A:Molecule type: protein
 A:Residues: 41-45 <ENG>
 A:Experimental source: normal urine
 R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
 Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
 A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
 A:Reference number: JC2404; MUID:95128033
 A:Accession: JC2404
 A:Molecule type: protein
 A:Residues: 41-53, 'X', '55-144, 'X', '146-150, 'X', '152-186, 'X', '188-201 <KAJ>
 A:Experimental source: urine
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
 C:Genetics:
 A:Gene: GDB:TNFR1
 A:Cross-references: GDB:125913; OMIM:191190
 A:Map position: 12p13.2-12p13.2
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>
 F:30-211/Domain: extracellular #status predicted <EXT>
 F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
 F:44-82/Domain: NGF receptor repeat homology <NGI>

F:84-126/Domain: NGF receptor repeat homology <NG2>
 F:127-167/Domain: NGF receptor repeat homology <NG3>
 F:168-196/Domain: NGF receptor repeat homology <NG4>
 F:212-234/Domain: transmembrane #status predicted <MEM>
 F:235-455/Domain: intracellular #status predicted <INT>
 F:34,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	99.0%	Score 1219;	DB 1;	Length 455;
Best Local Similarity	100.0%	Pred. No. 5.2e-82;		
Matches 217;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGLSTVPDLLPLVLLLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT	60	
Db	1	MGLSTVPDLLPLVLLLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISICT	60	
QY	61	KCHKGTLYNDPCPGQDTCRECEGSFTASENHLRHLCLSCSKCKRMGQVEISSCTVD	120	
Db	61	KCHKGTLYNDPCPGQDTCRECEGSFTASENHLRHLCLSCSKCKRMGQVEISSCTVD	120	
QY	121	RDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSQEKONTVCTCHAGFFLENECV	180	
Db	121	RDTVCGCRKNQYRHWSENLFQCFNCSLCLNGTVHLSQEKONTVCTCHAGFFLENECV	180	
QY	181	SCSNCKSLECTKLCPLQIENYKGTEDSGTTVLLPLV	217	
Db	181	SCSNCKSLECTKLCPLQIENYKGTEDSGTTVLLPLV	217	